

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 10, 2006, 05:49:50 ; Search time 4711 Seconds
(without alignments)
9941.386 Million cell updates/sec

Title: US-09-615-039-1_COPY_13000_14000

Perfect score: 1001

Sequence: 1 cgtccgacctggaggcagc.....ccccggagccttcaccacca 1001

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST: *
1: gb_est1: *
2: gb_est2: *
3: gb_est3: *
4: gb_hc: *
5: gb_est4: *
6: gb_est5: *
7: gb_est6: *
8: gb_est7: *
9: gb_gse1: *
10: gb_gse2: *
11: gb_gse3: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	291	29.1	409	7	CN274427 170005313
2	159.2	15.9	599	2	BB618671 BB618671
3	159.2	15.9	614	2	BB651920 BB651920
4	154.8	15.5	649	6	CF531069 UI-M-FY0-CF531069
5	154.8	15.5	688	6	CF531121 UI-M-FY0-CF531121
6	129.6	12.9	1523	10	AG448267 Mus muscu
7	127.2	12.7	1674	10	CL078342 CH216-149
8	127	12.7	1299	10	AG039481 Pan trogl
9	126.8	12.7	1690	10	AG435238 Mus muscu
10	126.2	12.6	1692	10	AG396765 Mus muscu
11	125.4	12.5	1661	10	AG435089 Mus muscu
12	125	12.5	1961	10	AG435522 Mus muscu
13	124.2	12.4	1168	3	BM468388 AGENCOURT
14	124.2	12.4	1552	10	AG430101 Mus muscu
15	124.2	12.4	1822	10	AG435170 Mus muscu
16	123.2	12.3	1355	10	AG429718 Mus muscu
17	121.6	12.1	1425	10	AG441757 Mus muscu
18	121	12.1	1628	10	CG757066 P052-2-A0
19	120.8	12.1	2243	10	AG381986 Mus muscu
20	120.8	12.1	1381	10	AG396965 Mus muscu
21	119.8	12.0	1218	10	CL081011 CH216-160
22	119.8	12.0	1302	10	AG448240 Mus muscu

C 23	119.8	12.0	1400	10	AG429585
C 24	119.8	12.0	1648	10	AG390465 Mus muscu
C 25	119.4	11.9	1096	5	BUB38702 AGENCOURT
26	119.2	11.9	1031	5	BUL167290 AGENCOURT
27	119	11.9	1713	10	AG435689 Mus muscu
28	118.6	11.8	1798	10	AG171124 Pan trogl
29	118.4	11.8	1288	5	BQ678719 AGENCOURT
C 30	118	11.8	1406	10	AG441598 Mus muscu
C 31	117.8	11.8	931	7	CK412737 AUF_IpG11
C 32	117.6	11.6	1392	10	AG390642 Mus muscu
C 33	116.4	11.6	1286	10	AG448422 Mus muscu
C 34	116.4	11.6	1713	10	AG435689 Mus muscu
C 35	116.2	11.6	2017	10	AG435283 Mus muscu
C 36	116	11.6	1341	10	AG030611 Pan trogl
C 37	116	11.6	1403	9	CC290252 CH261-172
38	115.8	11.6	1449	3	BM912953 AGENCOURT
39	115.2	11.5	1081	10	CL464716 SAIL-1225
40	115.2	11.5	1785	9	CC219595 CH261-62D
41	115	11.5	1212	3	BQ069498 AGENCOURT
C 42	115	11.5	1453	8	DN806685 76982446
C 43	114.6	11.4	1675	10	AG360980 Mus muscu
44	114.6	11.4	1694	10	CL509291 SAIL-811
45	114.4	11.4	1454	10	AG290167 Mus muscu

ALIGNMENTS

RESULT 1
CN274427

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

COMMENT

CN274427 409 bp mRNA linear EST 16-MAY-2004
17000531326763 GRN_ES Homo sapiens cDNA 5', mRNA sequence.

CN274427

CN274427.1 GI:47290841

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 409)

Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G. J.,

Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M. S., Mandalam, R.,

Lebkowski, J. and Stanton, L. W.

Transcriptome characterization elucidates signaling networks that

control human ES cell growth and differentiation

Nat. Biotechnol. 22 (6), 707-716 (2004)

15146197

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Regenerative Medicine

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Insert Length: 409 Std Error: 0.00.

FEATURES

Location/Qualifiers

1..409

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/tissue_type="embryonic stem cells, cell lines H1, H7, and

H9"

/clone_lib="GRN_ES"

/note="oligo dt primed, full-length enriched cDNA library

from undifferentiated hES cell lines H1 (p32), H7 (p29),

and H9 (p36) maintained in feeder-free conditions"

ORIGIN

Query Match

Best Local Similarity

Matches 305; Conservative

29.1%; Score 291; DB 7; Length 409;

98.1%; Pred. No. 7.4e-41;

0; Mismatches 5; Indels 1; Gaps 1;

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE AUTHORS

1 (bases 1 to 614)
Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Iehi, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sugabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, P., Takeda, Y., Tanaka, T., Toyota, T., Muramatsu, M. and Hayashizaki, Y.
RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
Unpublished (2001)

TITLE JOURNAL COMMENT

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Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL: <http://genome.gsc.riken.jp/>

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. *Genome Res.* 10 (10), 1617-1630 (2000)
wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multipipillary sequencer. *Genome Res.* 10 (11), 1757-1771 (2000)

Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. *Genome Res.* 11 (2), 281-289 (2001)

Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and Hayashizaki, Y.
Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences. *Mamm. Genome* 12, 673-677 (2001)

Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

FEATURES source

Location/Qualifiers
1. .614
/organism="Mus musculus"
/mol_type="mRNA"
/strain="CS7BL/6J"
/db_xref="taxon:10090"
/clone="C330020G14"
/cell_type="ES cells"
/lab_host="SOLR"
/clone_lib="RIKEN full-length enriched, ES cells"
/note="Site 1: XhoI; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN, Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5'
GAGAGAGAGATTCGAGTCTAATTAATTAATTCCTCCCCCCCC 3']"
GAGAGAGAGATTCGAGTCTAATTAATTAATTCCTCCCCCCCC 3']"

ORIGIN

Query Match 15.9%; Score 159.2; DB 2; Length 614;

Best Local Similarity 73.6%; Pred. No. 6.7e-18;
Matches 203; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

Qy 492 CAGCGCTCGCTCCGCTGGCGACGCTGGAGCCCTGGCCCGCCACCCCGCGATGCGG 551
Db 61 CACCTTTCGATCTTTGGTTCCCGACAGTGGAGGCCCATCCCGGCTTGAGCACATGACC 120
Qy 552 CGCGCTCCCGCTCCCGAGCGCGTCCGCTCCCTGCTGGCGCAGCCACTACCGCGAGGTGCTG 611
Db 121 CGCGCTCTCTGTTGCGCGCGGTGGCTCTCTGCTGGCGAGCCGATACCGGAGGTGG 180
Qy 612 CGCGTGGCCAGCTTGGTGGCGCGCTGGGGCCCCCAGGGCTGGCGGCTGGTGCAGGCGGG 671
Db 181 CGCGTGGCAACTTTGTGCGCGCGCTGGGGCCCCCAGGGCGAGGCGGCTTGTGCAACCCGG 240
Qy 672 GACCGCGGGCTTTCGCGCGCTGGTGGCGCGCTGGTGGCGCGCTGGTGGCGCGCTGGTGGCGCGCA 731
Db 241 GACCGGAGATCTACCGCACTTTGTGTCCTGTCCTAGTGTGATGCACTGGGGCTCA 300
Qy 732 CGCGCGCGCGCGCGCGCGCGCTCCCTCCCGCAGGTG 767
Db 301 CAGCTCCACCTGCGGACCTTCTCCACCGAGTG 336

RESULT 4

CF531069
LOCUS
DEFINITION
UI-M-FY0-cgp-c-19-0-UI.r1 NIH_BMAP_FY0 Mus musculus cDNA clone
IMAGE:30355746 5', mRNA sequence.

ACCESSION

CF531069

VERSION

CF531069.1 GI:34583033

KEYWORDS

EST.

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 649)
NIH-MSC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

REFERENCE

Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/mousef1.html>
This clone was contributed by the Brain Molecular Anatomy Project (BMAP)

Seq primer:

pyX-5.

Location/Qualifiers

1. .649
/organism="Mus musculus"
/mol_type="mRNA"
/strain="CS7BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:30355746"
/tissue_type="whole brain"
/dev_stage="embryo 13.5, 14.5, 16.5, 17.5dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH_BMAP_FY0"

note="Organ:

Brain; Vector: pYX-Asc; Site_1: EcoR I; Site 2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, *Genome Research*, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail

is AGCAGACAG. This library was created for the University Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

ORIGIN	Program Coordinates	Query Match	15.5%	Score 154.8;	DB 6;	Length 649;
		Best Local Similarity 78.2%;		Pred. No. 3.9e-17;		
		Matches 186; Conservative 0;		Mismatches 52;		Indels 0; Gaps 0;
QY	530	CCGCGGCCACCCCGCGATGCGCGCGCTCCCGCTGCGAGCGCTGCGCTCCCTGCTGCG	589			
Db	26	CCGCGCCTTGAGACATGACCGCGGCTCTCGTTGCCCGCGGTGCGCTCTCTGCTGCG	85			
QY	590	CAGCCACTACCGCGAGTGTCGCGCTGGCGCAAGTTCTGTCGGCGCTGCGGGCCCCAGGG	649			
Db	86	CAGCCGATACCGGAGGTGTGGCGCTGGCAACCTTTGTGCGCGCTGCGGGCCCCAGGG	145			
QY	650	CTGGCGCTGTCAGCGCGGGAGCCGGCGGCTTTCCGCGCGCTGTCGTCGCCAGATGCCCT	709			
Db	146	CAGCGCCTTGTGACCCGGGGACCCGAGATCTACCGCACTTGTGTCCTCATGCCCT	205			
QY	710	GGTGTGCGTCCCTGGACGACGCGCGCCCCCGCGCCCTCTCTCCGCCAGGTG	767			
Db	206	AGTGTGATGATCTGGGCTTCACAGCTTCACTGCGGACCTTTCCTTCACACAGGTG	263			

RESULT	5
CF531121	
LOCUS	
DEFINITION	
ACCESSION	
VERSION	
KEYWORDS	
SOURCE	
ORGANISM	
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
COMMENT	

size selected according to mRNA size fraction, ligated with EcoX I adaptor, digested with NotI and then cloned directionally into px-Asc vector. The library tag sequence located between the Not I site and the polyA tail is AGCGAGACAG. This library was created for the University of Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

ORIGIN	Query Match	15.5%;	Score 154.8;	DB 6;	Length 688;
	Best Local Similarity	78.2%;	Pred. No. 3.9e-17;		
	Matches 186;	Conservative 0;	Mismatches 52;	Indels 0;	Gaps 0;
Qy	530	CCGGCCACCCCGCGATGCGGCGCTCCCGCTGCGAGCGGTGCGCTCCCTGCTGCG	589		
Db	63	CCGGCCTTGAGCACATGACCCGCGCTCTCGTTGCCCGCGGTGCGCTCTCTGCTGCG	122		
Qy	590	CAGCCACTACCGGAGGTGTGCGGTGCGGCCACGTTCTGTGCGCGCGCTGTGGGCCCCAGGG	649		
Db	123	CAGCCGATACCGGAGGTGTGCGCGGTGCGCAACTTTGTGCGCGCGCTGTGGGCCCCAGGG	182		
Qy	650	CTGCGCGCTGGTCAGCGCGGGGACCCGGGGCTTTCCGCGCGCTGTTGGTGGCCCAAGTGCCT	709		
Db	183	CAGCGGCTTTGCAACCCGGGGACCCGAGATCTACCGCACATTTGGTTGCCCAATGCCT	242		
Qy	710	GGTGTGCGTCCCTGGGACGCA CGGCGGCCCCCGCGGCCCTCTCTTCGCGCAGGTG	767		
Db	243	AGTGTGATGCATGGGGTTCAGAGCTCCACCTGCGCGCACTTTCTTCCACCAAGGTG	300		

RESULT 6					
AG448267/c					
LOCUS	AG448267	1523 bp	DNA	linear	GSS 22-DEC-2004
DEFINITION	Mus musculus molossinus DNA, clone.MSMG01-332C15.TJ, genomic survey sequence.				

ACCESSION	AG48267				
VERSION	AG48267.1	GI:48091330			
KEYWORDS	GSS.				
SOURCE	Mus musculus molossinus	(Japanese wild mouse)			
ORGANISM	Mus musculus molossinus				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;				
	Sciurognathi; Muridae; Murinae; Mus.				
REFERENCE	1				
AUTHORS	Abe, K., Noguchi, H., Tagawa, K., Yuzuriha, M., Toyoda, A., Kojima, T.,				
	Ezawa, K., Saitou, N., Hattori, M., Sakaki, Y., Moriwaiki, K. and				
	Shiroishi, T.				

FEATURES	source
seq primer: p4x-3,	
Location/Qualifiers	
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/clone="IMAGE:30355988"	
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/dev_stage="embryo 13.5,14.5,16.5,17.5dpc"	
/lab_host="PH10B (T1 phage resistant)"	
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/note="Organ: Brain; Vector: pYX- Asc; Site 1: EcOR I; Site 2: Not 1; The library was constructed according Bonafido, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was	


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R.Site 1 : EcorI
R.Site 2 : EcorI.
Location/Qualifiers
1..1523
/organism="Mus musculus molossinus"
/mol_type="genomic DNA"
/sub_species="molossinus"
/db_xref="taxon:57486"
/clone="MSMG01-332C15.TJ"
/sex="male"
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FEATURES
Source
Query Match 12.9%; Score 129.6; DB 10; Length 1523;
Best Local Similarity 47.2%; Pred. No. 9.4e-13;
Matches 434; Conservative 0; Mismatches 479; Indels 6; Gaps 2;

QY 73 CCCAGGGCTCCACATCATGGCCCTCTCCCTCGGGTTACCCACAGCCTTAGGCCGATTGCA 132
DB 1185 CCCCAGGCCCCCGCGCGCCCCCGCGCCCCCGCGCCCCCGCGCCCCCGCGCCCCCGCG 1126
QY 133 CTTCTCTCGTGGGGCCCTCGTGGGCTCCTCTGACCTCTGGAGCGGAGCGGGCGG 192
DB 1125 CCGCCCGCGCGCCCCCGCGCCCCCGCGCCCCCGCGCCCCCGCGCCCCCGCGCCCC 1066
QY 193 GCGGGGAGCGGGCCAGACCCCGGGTCCGCGCGCGCGAGCAGCTGCGTGGGGCCA 252
DB 1065 CGCGCGCGCCCCCGCGCCCCCGCGCCCCCGCGCCCCCGCGCCCCCGCGCCCCCG 1006
QY 253 GCGCGGCTCCAGTGATTGCGGGGACAGACGCCAGAGACCGCGCTTCCACAGTGCGG 312
DB 1005 GCCCCGCGCGCGCGCGCCCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 946
QY 313 GAGGACTGGGAGCCCGGGACCGCGTCTGCGCCCTTCACTTCAGCTTCGCTCTCGG 372
DB 945 CCGCGCCCCCGCGCGCCCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 886
QY 373 CGCGAGCCCCCGCGCGTCCGACCCCTCCCGGGTCCCGGGCCAGCCCTTCGGGGCCT 432
DB 885 CCGCGCGCCCCCGCGCGCGCCCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 826
QY 433 CCGAGCCCTCCCTTCTTCGCGGGCCCGCGCTCTCTCTCTCTCTCTCTCTCTCTCT 492
DB 825 CCCCCCCCCCGCGCGCCCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 766
QY 493 AGCGTGGCTCTGTCGCGACAGTGGGGAAGCCCTGCGCCCGCGCCACACCCCGCATGCGCG 552
DB 765 CCCCCCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 706
QY 553 GCGTTCCTCCGTCGCGAGCGTGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 612
DB 705 CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 646
QY 613 CGTGGCCACGTTCTGCGGGGCGCTTGGGGCCCCAGGCGTGGCGTGGTGGAGCGGG 672
DB 645 GCGCCCCCCCCCGCGCCCCCCCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 586
QY 673 ACCCGCGCGCTTTCGCGCGCTGGTGGGCGCAGTGGCTGGTGGCTGGGACGCGAC 732
DB 585 CCGCTTCGCGGCCCCCGCGGCCCCCCCCCGCGCCCCCGCGCCCCCGCGCCCCCG 526
QY 733 GCGCCCGCCCCCGCGCCCCCTCTCTTCGCGCAGGTGGGCTTCCCGGGGTGGCGTTCGGG 792
DB 525 GGGCCCCCCCCCGCGCCCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 466
QY 793 TGGGGTGGGGCGCGCGGGGGGAACGAG--CGACATGGGAGAGAGCGGCGAGGCGCTC 850
DB 465 CCGCGCCCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 406
QY 851 AGGGCGCTTCCCCCGCAGGTGCTCTGTAAGAGAGCTGGTGGC---CCGAGTGTGCA 906
DB 405 CCGGGCCCCCCCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 346
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QY 907 GAGGCTGTGCGAGCGCGCGCGGAGAACGTGTGGCTTCGGCTTCGGCTGTGGACGG 966
DB 345 GCCGCCCGCGCGCGCGCGCGCCGCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCC 286
QY 967 GGCGCGCGGGGGGCCCCCCCC 985
DB 285 CCGCGCGCGCGCGCGCGCGCCCC 267

RESULT 7
LOCUS CL078342 1674 bp DNA linear GSS 31-DEC-2003
DEFINITION CH216-149D22 Sp6.1 CH216 Xenopus tropicalis genomic clone
CH216-149D22, genomic survey sequence.
VERSION CL078342
KEYWORDS CL078342.1 GI:40534255
SOURCE GSS.
ORGANISM Xenopus tropicalis (western clawed frog)
Xenopus tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
Xenopodinae; Xenopus; Silurana.
REFERENCE 1 (bases 1 to 1674)
AUTHORS Kremitzki,C., Carter,J., McPherson,J., Warren,W., Graves,T.,
Mardis,E. and Wilson,R.
TITLE A physical map of the xenopus tropicalis genome
JOURNAL Unpublished (2003)
COMMENT Contact: Richard K Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Insert Length: 175000 Std Error: 0.00
Seq primer: Sp6 ATTTAGGTGACACTATAG
Class: BAC ends
High quality sequence start: 300
High quality sequence stop: 387.

FEATURES
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/sex="male"
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/note="Vector: pTARBAC.1; CHORI-216 Xenopus tropicalis
BAC library"
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QY 64 GCACCTGTTCACAGGCGCTCCACATCATGGCCCTCTCCCTCGGGTTACCCACAGCTAGG 123
DB 676 CCGCGCCCCCGCGCGCCCCCGCGCCCCCGCGCGCGCGCGCGCGCGCGCGCGCG 735
QY 124 CCGATTGACCTCTCTCTGGGGGCGCTCTCGCTGGCGTCTCTGACCTCTGGAGGCGGAG 183
DB 736 GCGCCCCCGCGCGCCCCCGCGCCCCCGCGCCCCCGCGCCCCCGCGCCCCCGCGCG 795
QY 184 CCGCGCGCGGGGAGCGCGGCCAGAGACCCCGGGTCCCGCGGAGAGCTGCGCTG 243
DB 796 CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 855
QY 244 TCGGGCGCGCGCGCTCCAGTGGATTTCGGGCGGACAGACGCGCGCGCGCGCGCG 303
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS

1 Abe, K., Noguchi, H., Tagawa, K., Yuzuriha, M., Toyoda, A., Kojima, T., Ezawa, K., Saitou, N., Hattori, M., Sakaki, Y., Moriwaki, K. and Shiroishi, T.

TITLE

Contribution of Asian mouse subspecies *Mus musculus molossinus* to genomic constitution of strain C57BL/6J, as defined by BAC-end

JOURNAL
PUBMED

Genome Res. 14 (12), 2439-2447 (2004)

REFERENCE
AUTHORS

2 (bases 1 to 1692)

TITLE

Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.
Direct Submission
Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail: hattori@psc.riken.jp, URL: http://hgp.gsc.riken.go.jp/, Tel: 81-45-503-9111, Fax: 81-45-503-9170)

COMMENT

Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
Tsukuba Institute, Bio Resource Center,
The Institute of Physical and Chemical Research (RIKEN) 3-1-1 Koyadai, Tsukuba, 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
e-mail: abe@rtc.riken.jp

Sequencing : TJ

LIBRARY

Vector : pBACe3.6

R.Site 1 : EcoRI

R.Site 2 : EcoRI

FEATURES
source

Location/Qualifiers

1. .1692

/organism="Mus musculus molossinus"

/mol_type="genomic DNA"

/sub_species="molossinus"

/db_xref="taxon:57486"

/clone="MSMg01-217C03.TJ"

/sex="male"

/tissue type="mixture of kidney and spleen"

/clone_lib="MSMg01 Mouse Male BAC Library"

ORIGIN

Query Match 12.6%; Score 126.2; DB 10; Length 1692;

Best Local Similarity 47.0%; Pred. No. 3.7e-12;

Matches 433; Conservative 0; Mismatches 485; Indels 3; Gaps 2;

Qy 80 CCTCCACATCATGCCCCCTCTCGGGTATACCCACAGCCTAGGCGGATTCGACCTCTCT 139

Db 1526 CCCCCCGCCCCCGCCCCCCCCCCCCCGCCGCGCCGCCCCCGCCGCCCCCGCCGCGC 1467

Qy 140 CCGCTGGGGCCCTCGCTGGCGCTCTCTGCACCTGGGAGCGGACGCGCGGGCGGG 199

Db 1466 GCGCGCGCCCGCGCCCGCGCCCGCGCCCGCCCGCGCGCGCGCGCGCGCGCGCC 1407

Qy 200 AAGCGCGCCCGAGACCCCGGGTCCGCGCGGAGCAGCTGCGCTGTCGGGGCGAGCGCGG 259

Db 1406 GCGCGCGCCCGCGCCCGCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCC 1347

Qy 260 CTCCAGTGGATTGCGGGGACACAGCGCCAGGACCGGCTTCCACGTGGGAGGAGAC 319

Db 1346 CCCCCCGCCCCCGCGCGGCGGCGCCCGCCCCCGCCCCCGCCCCCGCCCCCGCCCC 1287

Qy 320 TGGGGACCCCGGACCCCGTCTCTGCGCTTACCTTCAGCTTCGCGCTCTCCCGCGCGGAC 379

Db 1286 CGCCCCCGCCCCCGGGCGCCCGCGCCCGCCCGCGCCCGCCCGCCCGCCCGCCCGC 1228

Qy 380 CCGCGCCCGCTCCGACCCCTCTCCGGGTCCCGGGTCCCGGGCCAGCCCCCTTCGGGGCC 439

Db 1227 CCCCCCGCGCCCCCGCCCCCGCCCCCGCCCCCGCCCCCGCCCCCGCCCCCGCCCC 1168

Qy 440 CTTCCCTCTCTTTTCGGGCGCCCGCCCTCTCTCTCGGCGCGAGTTTTCAGGAGCGCTG 499

Db 1167 CGCCCCCCCCCCCCCGCGCCCCCCCCCGCGCCGCGCCCCCCCCCCCCCCCCCGCGCG 1108

Qy 500 CGTCTCTGCTCGCACGCTGGGAAGCCCTTGGCCCGCGGCACACCCCGATGCGCGCGCTCC 559

Db 1107 CGCGCCCGCCCGCCCGCCCGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1048

Qy 560 CGGTCGCGAGCGTGGCTCTCTGTCGCGACGACACTACCGGAGAGTGTGCGGCTGGCG 619

Db 1047 CCGCGCGCCCG 990

Qy 620 CAGTTCGTCGCGGCGCTGGGGCCCGAGGCTGCGCGCTGTCAGCGCGGAGACCGCGC 679

Db 989 CCGCGCCCGCCCGCCCGCCCGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 930

Qy 680 GGCTTTTCGCGCGCTGTGTGCGCCCGAGTGTCTGTGTGTGTCGTCCTTGGGACGACGCGCG 739

Db 929 GCGGCGCCCGCCCGCCCGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 870

Qy 740 CCGCGCGCCCGCTCTCTCTGTCGCGAGTGGGCTCTCCCGGGTGTGCGGCTGGGGTT 799

Db 869 CCG 810

Qy 800 GAGGCGCGCGGGGGAACCGAGGACATGCGGAGAGCGAGCGAGGCGAGCTCAGGGCGCTT 859

Db 809 CCG 750

Qy 860 CCGCGCGAGGTGTCTCTGCTGAAGAGAGTGTGTGCGCGCGAGTGTGACAGAGGCTGTGCGAG 919

Db 749 CCGCGCCCGCCCG 690

Qy 920 CGCGCGCGGAGAAAGTGTGCGCTCTGCGGCTTCTGCGCTGTGACGCGGGGCGCGCGGGCG 979

Db 689 CCG 630

Qy 980 CCGCGCGAGGCGCTTCAACCACC 1000

Db 629 CCG 609

RESULT 11
AG435089/c
LOCUS
DEFINITION Mus musculus molossinus DNA, clone:MSMg01-313A16.TJ, genomic survey sequence.
ACCESSION AG435089
VERSION AG435089.1 GI:48078152
KEYWORDS GSS.
SOURCE Mus musculus molossinus (Japanese wild mouse)
ORGANISM Mus musculus molossinus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Abe, K., Noguchi, H., Tagawa, K., Yuzuriha, M., Toyoda, A., Kojima, T., Ezawa, K., Saitou, N., Hattori, M., Sakaki, Y., Moriwaki, K. and Shiroishi, T.
TITLE Contribution of Asian mouse subspecies *Mus musculus molossinus* to genomic constitution of strain C57BL/6J, as defined by BAC-end sequence-SNP analysis
JOURNAL Genome Res. 14 (12), 2439-2447 (2004)
PUBMED 15574823
REFERENCE 2 (bases 1 to 1692)
AUTHORS Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.
TITLE Direct Submission
JOURNAL Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail: hattori@psc.riken.jp, URL: http://hgp.gsc.riken.go.jp/, Tel: 81-45-503-9111, Fax: 81-45-503-9170)
COMMENT Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp).

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 10, 2006, 11:12:13 ; Search time 210.333 Seconds
(without alignments)
3469.703 Million cell updates/sec

Title: US-09-615-039-1_COPY_13000_14000
Perfect score: 1001
Sequence: 1 cgtccgacctggaggcagc.....ccccggagcctccaccacca 1001

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4637633 seqs, 364532575 residues

Total number of hits satisfying chosen parameters: 9275266

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA New:*

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- 2: /cgm2_6/ptodata/1/pubna/US06_NEW_PUB.seq.*
- 3: /cgm2_6/ptodata/1/pubna/US07_NEW_PUB.seq.*
- 4: /cgm2_6/ptodata/1/pubna/PCT_NEW_PUB.seq.*
- 5: /cgm2_6/ptodata/1/pubna/US09_NEW_PUB.seq.*
- 6: /cgm2_6/ptodata/1/pubna/US10_NEW_PUB.seq.*
- 7: /cgm2_6/ptodata/1/pubna/US11_NEW_PUB.seq.*
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- 9: /cgm2_6/ptodata/1/pubna/US11_NEW_PUB.seq.*
- 10: /cgm2_6/ptodata/1/pubna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	412.4	41.2	496	7	US-11-096-622-18
C 2	412.4	41.2	8565	7	US-11-096-622-21
C 3	397	39.7	397	7	US-11-066-480-2
4	259.4	25.9	261	6	US-10-863-093-24
5	259.4	25.9	295	6	US-10-140-776A-4
6	259.4	25.9	295	6	US-10-140-776A-5
7	259.4	25.9	5928	6	US-10-863-093-25
8	247	24.7	2038	7	US-11-066-480-9
9	244	24.4	245	7	US-11-066-480-3
10	242.2	24.2	2041	7	US-11-066-480-11
11	78	7.8	78	6	US-10-863-093-7
C 12	74.2	7.4	170595	7	US-11-121-086-35
C 13	69.6	7.0	153376	7	US-11-121-086-5
C 14	68.6	6.9	268685	6	US-10-933-025-22
C 15	67.4	6.7	1557	7	US-10-996-217A-6
C 16	67	6.7	5679	7	US-11-075-185-36
17	67	6.7	78869	7	US-11-075-185-1
18	67	6.7	191684	7	US-11-121-086-2
C 19	64.8	6.5	180654	7	US-11-121-086-58
C 20	64.2	6.4	2562	7	US-11-052-554A-533
C 21	64	6.4	25257	6	US-10-995-561-13412
C 22	64	6.4	171936	6	US-10-933-025-24
C 23	64	6.4	220895	6	US-10-775-169-88

C 24	63.4	6.3	191684	7	US-11-121-086-2	Sequence 2, Appli
25	63	6.3	26000	6	US-10-949-720-391	Sequence 391, App
26	62	6.2	46752	6	US-10-995-561-13410	Sequence 13410, A
27	62	6.2	415117	6	US-10-995-561-13274	Sequence 13274, A
28	60.6	6.1	150468	7	US-11-112-908-56	Sequence 56, Appl
29	60.6	6.1	193789	7	US-11-112-908-55	Sequence 55, Appl
30	60.4	6.0	2750	6	US-10-131-826A-85	Sequence 85, Appl
C 31	60.4	6.0	5706	7	US-11-052-554A-519	Sequence 519, App
C 32	59.4	5.9	150481	7	US-11-112-908-37	Sequence 37, Appl
C 33	59.4	5.9	171162	7	US-11-112-908-38	Sequence 38, Appl
C 34	59.4	5.9	1080000	6	US-10-928-446A-1	Sequence 1, Appli
C 35	59.4	5.9	1080000	6	US-10-928-446A-181	Sequence 181, App
C 36	59.4	5.9	1080000	6	US-10-928-446A-183	Sequence 183, App
C 37	59.4	5.9	1080000	6	US-10-928-446A-185	Sequence 185, App
C 38	59.4	5.9	1080000	6	US-10-928-446A-187	Sequence 187, App
C 39	59.4	5.9	1080000	6	US-10-928-446A-189	Sequence 189, App
C 40	59.4	5.9	1080000	6	US-10-928-446A-191	Sequence 191, App
C 41	59.4	5.9	1080000	6	US-10-928-446A-193	Sequence 193, App
C 42	59.4	5.9	1080000	6	US-10-928-446A-195	Sequence 195, App
C 43	59.4	5.9	1080000	6	US-10-928-446A-197	Sequence 197, App
C 44	59.4	5.9	1080000	6	US-10-928-446A-199	Sequence 199, App
C 45	59.4	5.9	1080000	6	US-10-928-446A-201	Sequence 201, App

ALIGNMENTS

RESULT 1

US-11-096-622-18/c
; Sequence 18, Application US/11096622
; Publication No. US2005026043A1
; GENERAL INFORMATION:
; APPLICANT: HUNG, MIEN-CHIE
; APPLICANT: DAY, CHI-PING
; APPLICANT: RAY, KUN-MING
; APPLICANT: XIE, XIAOMING
; APPLICANT: LI, ZHENG
; TITLE OF INVENTION: CANCER SPECIFIC PROMOTERS
; FILE REFERENCE: UTSC:845US
; CURRENT APPLICATION NUMBER: US/11/096,622
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: 60/559,111
; PRIOR FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 18
; LENGTH: 496
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
US-11-096-622-18

Query Match 41.2%; Score 412.4; DB 7; Length 496;
Best Local Similarity 98.4%; Pred. No. 7.1e-52;
Matches 427; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

Qy	92	GGCCCTCCCTCGGGTTACCCACAGCCTAGCCGATTCGACCTCTCTCCGCTGGGGCCC	151
Db	433	GGCCCTCCCTCGGGTTACCCACAGCCTAGCCGATTCGACCTCTCTCCGCTGGGGCCC	374
Qy	152	TGCTGGGGTCCCTCGACCTCGGGAGCCGAGCCGCGGGGGAAGCGCGGCCCA	211
Db	373	TGCTGGGGTCCCTCGACCTCGGGAGCCGAGCCGCGGGGGAAGCGCGGCCCA	314
Qy	212	GACCCCGGGTCCCGCCCGAGCAGCTGGCTGTTCGGGGCCAGCGCGGCTCCCACTGGAT	271
Db	313	GACCCCGGGTCCCGCCCGAGCAGCTGGCTGTTCGGGGCCAGCGCGGCTCCCACTGGAT	254
Qy	272	TGCGGGGACAGAGCCCGCAGACCGCGCTTCCCACTGGGGAGGGAATGGGGACCCGGG	331
Db	253	TGCGGGGACAGAGCCCGCAGACCGCGCTTCCCACTGGGGAGGGAATGGGGACCCGGG	194

QY 332 CACCGTCTCCGCGCTTACCTTCCAGCTCCGCTCCGCTCCGCGGAGACCCGCGCTCC 391
Db 193 CACCGTCTCCGCGCTTACCTTCCAGCTCCGCTCCGCTCCGCGGAGACCCGCGCTCC 134
QY 392 CGACCCCTCCGCGGTCCTCCGCGGAGCCCTCCGCGGAGCCCTCCGCGGAGCCCTCCGCTCC 451
Db 133 CGACCCCTCCGCGGTCCTCCGCGGAGCCCTCCGCGGAGCCCTCCGCGGAGCCCTCCGCTCC 75
QY 452 TTCGCGGCGCCGCGCTTCCGCGGAGCCCTCCGCGGAGCCCTCCGCGGAGCCCTCCGCTCC 511
Db 74 TTCGCGGCGCCGCGCTTCCGCGGAGCCCTCCGCGGAGCCCTCCGCGGAGCCCTCCGCTCC 15
QY 512 CACGTGGGAAGCC 525
Db 14 CACGTGGGGCGGCC 1
RESULT 2
US-11-096-622-21/c
; Sequence 21, Application US/11096622
; Publication No. US20050260643A1
; GENERAL INFORMATION:
; APPLICANT: HUNG, MIEN-CHIE
; APPLICANT: DAY, CHI-PING
; APPLICANT: RAU, KUN-MING
; APPLICANT: XIE, XIAOMING
; APPLICANT: LI, ZHENG
; TITLE OF INVENTION: CANCER SPECIFIC PROMOTERS
; FILE REFERENCE: UTSC:845US
; CURRENT APPLICATION NUMBER: US/11/096,622
; PRIOR FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: 60/559,111
; PRIOR FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 8565
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-096-622-21
Query Match 41.2%; Score 412.4; DB 7; Length 8565;
Best Local Similarity 98.4%; Pred. No. 3.5e-52;
Matches 427; Conservative 0; Mismatches 6; Indels 1; Gaps 1;
QY 92 GGCGCTCCCTCCGCGTACCCACAGCTAGCCGATTCGACCTCTCCGCTGGGGCC 151
Db 1772 GGCGCTCCCTCCGCGTACCCACAGCTAGCCGATTCGACCTCTCCGCTGGGGCC 1713
QY 152 TCCTGGCGTCCCTGCACCTCCGAGCGAGCGCGCGCGGGGAGCGGCGCCCA 211
Db 1712 TCCTGGCGTCCCTGCACCTTCGGAGCGAGCGCGCGGGGAGCGGCGCCCA 1653
QY 212 GACCCCGCGTCCGCGGAGCAGCTGCTGTTCGGGCGCAGCGCGGCTCCAGTGGAT 271
Db 1652 GACCCCGCGTCCGCGGAGCAGCTGCTGTTCGGGCGCAGCGCGGCTCCAGTGGAT 1593
QY 272 TCGGGGGACAGACCGCCAGACCGCTTCCAGCTCCGCTCCGCGGAGGAGCTGGGACCGGG 331
Db 1592 TCGGGGGACAGACCGCCAGACCGCTTCCAGCTCCGCTCCGCGGAGGAGCTGGGACCGGG 1533
QY 332 CACCGTCTCCGCGCTTACCTTCCAGCTCCGCTCCGCGGAGACCCGCGCTCC 391
Db 1532 CACCGTCTCCGCGCTTACCTTCCAGCTCCGCTCCGCGGAGACCCGCGCTCC 1473
QY 392 CGACCCCTCCGCGGTCCTCCGCGGAGCCCTCCGCGGAGCCCTCCGCGGAGCCCTCCGCTCC 451
Db 1472 CGACCCCTCCGCGGTCCTCCGCGGAGCCCTCCGCGGAGCCCTCCGCGGAGCCCTCCGCTCC 1414

QY 452 TTCGCGGCGCCGCGCTTCCAGCTCCGCTCCGCGGAGGATTTTCAGGCGAGCTCCGCTCCGCTCCG 511
Db 1413 TTCGCGGCGCCGCGCTTCCAGCTCCGCTCCGCGGAGGATTTTCAGGCGAGCTCCGCTCCGCTCCG 1354
QY 512 CACGTGGGAAGCC 525
Db 1353 CACGTGGGGCGGCC 1340
RESULT 3
US-11-066-480-2
; Sequence 2, Application US/11066480
; Publication No. US20050282280A1
; GENERAL INFORMATION:
; APPLICANT: ENNIST, DAVID LEONARD
; TITLE OF INVENTION: ONCOLYTIC ADENOVIRAL ENCODING GM-CSF
; FILE REFERENCE: GTIN-001
; CURRENT APPLICATION NUMBER: US/11/066,480
; CURRENT FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: US/10/925,205
; PRIOR FILING DATE: 2004-08-23
; PRIOR APPLICATION NUMBER: 60/499,312
; PRIOR FILING DATE: 2003-08-28
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 397
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-066-480-2
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Best Local Similarity 100.0%; Pred. No. 1.2e-49;
Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 CCCTCGTGGCGTCCCTGACACCTTGGGAGCGAGCGCGCGGGGAGCGGGGAGCGGGC 60
QY 209 CCAGACCCCGGGTCCGCGGAGCAGCTGCTGTTCGGGCGCAGGCGCGGCTCCAGTG 268
Db 61 CCAGACCCCGGGTCCGCGGAGCAGCTGCTGTTCGGGCGCAGGCGCGGCTCCAGTG 120
QY 269 GATTGGGGGACAGACCGCCAGACCGCTTCCACGTTGGCGGAGGAGCTGGGAGCC 328
Db 121 GATTGGGGGACAGACCGCCAGACCGCTTCCACGTTGGCGGAGGAGCTGGGAGCC 180
QY 329 GGGCACCCGCTCCGCGCTTCACTTCAGCTCCGCTCCGCGGAGACCCGCGCGCG 388
Db 181 GGGCACCCGCTCCGCGCTTCACTTCAGCTCCGCTCCGCGGAGACCCGCGCGCG 240
QY 389 TCCGACCCCTCCGCGGTCCCGGCGCAGCCCTTCGCGGCGCTTCAGGCGGCTCCGCT 448
Db 241 TCCGACCCCTCCGCGGTCCCGGCGCAGCCCTTCGCGGCGCTTCAGGCGGCTCCGCT 300
QY 449 CTTTTCGCGGCGCGCGCTTCCTTCGCGGCGGAGGTTTCAGGCGGCTTCGCT 508
Db 301 CTTTTCGCGGCGCGCGCTTCCTTCGCGGCGGAGGTTTCAGGCGGCTTCGCT 360
QY 509 GCGCAGCTGGGAGACCCCTGCGCCCGCGGACCCCGCG 545
Db 361 GCGCAGCTGGGAGACCCCTGCGCCCGCGGACCCCGCG 397
RESULT 4
US-10-863-093-24
; Sequence 24, Application US/10863093
; Publication No. US20050269081A1
; GENERAL INFORMATION:
; APPLICANT: Andrews, William H.
; APPLICANT: Foster, Christopher A.
; APPLICANT: Fraser, Stephanie
; APPLICANT: Mohammadpour, Hamid

		TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING	
		TITLE OF INVENTION: TELOMERASE REVERSE TRANSCRIPTASE (TERT) EXPRESSION	
		FILE REFERENCE: SIER-005	
		CURRENT APPLICATION NUMBER: US/10/863,093	
		PRIOR FILING DATE: 2004-06-08	
		PRIOR APPLICATION NUMBER: US/09/932,581	
		PRIOR FILING DATE: 2001-08-17	
		PRIOR APPLICATION NUMBER: 60/227,865	
		PRIOR FILING DATE: 2000-08-24	
		PRIOR APPLICATION NUMBER: 60/230,174	
		PRIOR FILING DATE: 2000-09-01	
		PRIOR APPLICATION NUMBER: 60/238,345	
		PRIOR FILING DATE: 2000-10-05	
		NUMBER OF SEQ ID NOS: 25	
		SOFTWARE: FastSeq for Windows Version 4.0	
		SEQ ID NO 24	
		LENGTH: 261	
		TYPE: DNA	
		ORGANISM: human	
		US-10-863-093-24	
		Query Match	25.9%; Score 259.4; DB 6; Length 261;
		Best Local Similarity	99.6%; Pred. No. 8.5e-30;
		Matches 260; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
Qy	288	CCAGGACCGCGCTTTCCACGTGGCGGAGGGAAGTGCGGACCCCGGCCTCTCCGCCCT	347
Db	1	CCAGGACCGCGCTCCCCACGTGGCGGAGGACTGCGGACCCCGGCCTCTCCGCCCT	60
Qy	348	TCACCTTCCAGCTCGGCTCTCTCGCGGGAGACCCTCCGACCCCTCCCGGGTC	407
Db	61	TCACCTTCCAGCTCGGCTCTCTCGCGGGAGACCCTCCGACCCCTCCCGGGTC	120
Qy	408	CCCGGCCACGAGCCCTCTCGGGCCCTCCAGAGCCCTCCGCTTCTTTCGCGGCCCGGCC	467
Db	121	CCCGGCCACGAGCCCTCTCGGGCCCTCCAGAGCCCTCCGCTTCTTTCGCGGCCCGGCC	180
Qy	468	TCTCCTCGCGCGGAGTTTCAGGCAGCGCTCGCTCTGCTGCGCACGTGGGAAGCCCTG	527
Db	181	TCTCCTCGCGCGGAGTTTCAGGCAGCGCTCGCTCTGCTGCGCACGTGGGAAGCCCTG	240
Qy	528	GCCC GCCGACCCCGCGATG	548
Db	241	GCCC GCCGACCCCGCGATG	261
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		US-10-140-776A-4	
		; Sequence 4, Application US/10140776A	
		; Publication No. US20050250186A1	
		; GENERAL INFORMATION:	
		; APPLICANT: Andrews, William H.	
		; APPLICANT: Foster, Christopher	
		; APPLICANT: Fraser, Stephanie	
		; APPLICANT: Mohammadpour, Hamid	
		; TITLE OF INVENTION: Methods and Compositions for Modulating	
		; TITLE OF INVENTION: Telomerase Reverse Transcriptase (TERT) Expression	
		; FILE REFERENCE: SIER-013	
		; CURRENT APPLICATION NUMBER: US/10/140,776A	
		; CURRENT FILING DATE: 2202-05-07	
		; PRIOR APPLICATION NUMBER: 60/289,717	
		; PRIOR FILING DATE: 2001-05-08	
		; NUMBER OF SEQ ID NOS: 5	
		; SOFTWARE: FastSeq for Windows Version 4.0	
		; SEQ ID NO 4	
		; LENGTH: 295	
		; TYPE: DNA	
		; ORGANISM: human	
		; FEATURE:	
		; OTHER INFORMATION: oligonucleotide	
		US-10-140-776A-4	
		Query Match	25.9%; Score 259.4; DB 6; Length 295;

RESULT 7
US-10-863-093-25
; Sequence 25, Application US/10863093
; Publication No. US20050269081A1
; GENERAL INFORMATION:
; APPLICANT: Andrews, William H.
; APPLICANT: Foster, Christopher A.
; APPLICANT: Fraser, Stephanie
; APPLICANT: Mohammadpour, Hamid
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING
; FILE REFERENCE: SIER-005
; CURRENT APPLICATION NUMBER: US/10/863,093
; CURRENT FILING DATE: 2004-06-08
; PRIOR APPLICATION NUMBER: US/09/932,581
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/227,865
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 60/230,174
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/238,345
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: RastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 5928
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic expression plasmid
US-10-863-093-25
Query Match 25.9%; Score 259.4; DB 6; Length 5928;
Best Local Similarity 97.8%; Pred. No. 3.9e-30;
Matches 263; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 288 CCAGACCGCGCTCCACAGTGGGGAGGAGTGGGACCGGGGACCGCTCTGCGCCT 347
Db 38 CCAGACCGCGCTCCACAGTGGGGAGGAGTGGGACCGGGGACCGCTCTGCGCCT 97
Qy 348 TCACCTTCAGCTCGCGCTCTCCGCGGACCGCGCGCTCCGACCCCTCCGGGTC 407
Db 98 TCACCTTCAGCTCGCGCTCTCCGCGGACCGCGCGCTCCGACCCCTCCGGGTC 157
Qy 408 CCGCGCCAGCCCTCCGCGGCTCCAGGCTCCAGGCTCCGCTTCCTTCGCGGCGCCGCC 467
Db 158 CCGCGCCAGCCCTCCGCGGCTCCAGGCTCCAGGCTCCGCTTCCTTCGCGGCGCCGCC 217
Qy 468 TCTCTCGCGGCGAGTTTACGAGCGCTGCGTCTGCTGCGGAGGAGCCCTG 527
Db 218 TCTCTCGCGGCGAGTTTACGAGCGCTGCGTCTGCTGCGGAGGAGCCCTG 277
Qy 528 GCGCGGCGACCGCGGATCGCGCGC 556
Db 278 GCGCGGCGACCGCGGATCGCGCGC 306

RESULT 8
US-11-066-480-9
; Sequence 9, Application US/11066480
; Publication No. US2005028280A1
; GENERAL INFORMATION:
; APPLICANT: ENNIST, DAVID LEONARD
; TITLE OF INVENTION: ONCOLYTIC ADENOVIRAL ENCODING GM-CSF
; FILE REFERENCE: GTIN-001
; CURRENT APPLICATION NUMBER: US/11/066,480
; CURRENT FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: US/10/925,205
; PRIOR FILING DATE: 2004-08-23
; PRIOR APPLICATION NUMBER: 60/499,312
; PRIOR FILING DATE: 2003-08-28

; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 2038
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: 1 to 2038 of Ar20-1006 including an ITR, packaging signal, poly A
; OTHER INFORMATION: , hTERT promoter, E1a gene and a portion of the E1b gene.
US-11-066-480-9

Query Match 24.7%; Score 247; DB 7; Length 2038;
Best Local Similarity 96.2%; Pred. No. 3.1e-28;
Matches 253; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
Qy 284 AGCCACAGACCGCGCTTCCACGTGGCGAGGAGTGGGACCGGGGACCGCTCTGTC 343
Db 529 ATGTCTGATCCGCTAGCCCACTGGCGAGGAGTGGGACCGGGGACCGCTCTGTC 588
Qy 344 CCCTTCACCTTCCAGCTCCGCTCTCCGCGGAGACCGCGCGCTCCGACCCCTCCG 403
Db 589 CCCTTCACCTTCCAGCTCCGCTCTCCGCGGAGACCGCGCGCTCCGACCCCTCCG 648
Qy 404 GGTCCCGCGCCAGCCCTCCGCGGCTCCAGGCTCCGCTTCCTTCCTTCCTTCCTTC 463
Db 649 GGTCCCGCGCCAGCCCTCCGCGGCTCCAGGCTCCGCTTCCTTCCTTCCTTCCTTC 708
Qy 464 GCGCTCTCTCGCGGCGAGTTTACGAGCGCTGCTGCTGCGGAGGAGGAGGAGGAGC 523
Db 709 GCGCTCTCTCGCGGCGAGTTTACGAGCGCTGCTGCTGCGGAGGAGGAGGAGGAGC 768
Qy 524 CCGCGCGCGCCACCCCGCGA 546
Db 769 CCGCGCGCGCCACCCCGCGA 791

RESULT 9
US-11-066-480-3
; Sequence 3, Application US/11066480
; Publication No. US2005028280A1
; GENERAL INFORMATION:
; APPLICANT: ENNIST, DAVID LEONARD
; TITLE OF INVENTION: ONCOLYTIC ADENOVIRAL ENCODING GM-CSF
; FILE REFERENCE: GTIN-001
; CURRENT APPLICATION NUMBER: US/11/066,480
; CURRENT FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: US/10/925,205
; PRIOR FILING DATE: 2004-08-23
; PRIOR APPLICATION NUMBER: 60/499,312
; PRIOR FILING DATE: 2003-08-28
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 245
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-066-480-3

Query Match 24.4%; Score 244; DB 7; Length 245;
Best Local Similarity 100.0%; Pred. No. 1.4e-27;
Matches 244; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 302 CCACAGTGGCGGAGGAGTGGGACCGGGGACCGGCTTCCTTCCTTCCTTCCTTCCT 361
Db 2 CCACAGTGGCGGAGGAGTGGGACCGGGGACCGGCTTCCTTCCTTCCTTCCTTCCTTC 61
Qy 362 GCGCTCTCTCGCGGAGACCGCGCCCTCCCGACCCCTCCCGGCTCCCGGCGCCAGGCC 421
Db 62 GCGCTCTCTCGCGGAGACCGCGCCCTCCCGACCCCTCCCGGCTCCCGGCGCCAGGCC 121
Qy 422 CTCGCGGCGCTTCACAGCCCTTCCTTCCTTCCTTCGCGGCGCCGCTTCCTTCCTTC 481
Db 122 CTCGCGGCGCTTCACAGCCCTTCCTTCCTTCCTTCGCGGCGCCGCTTCCTTCCTTC 181

Db 106092 GCCCGCGCTGCGATGTTCTGGCGCGCCCTAGCCGAGGATGCTGAGGATGAAGCTGCCGCTG 106033
Qy 501 GTCTGTGCGCAGTGGGAAGCCCTTGGCCCGCCGACACCCCGCGATGCGCGCGCTCCC 560
Db 106032 AAGCAACGCAACCCCGCGAGCCCGCCCGAGCGGAGAGCCCGAGCGGAGCGCGG 105973
Qy 561 GCCTGCGGAGCGGTGCGCTCCCTGCGAGCCACTACGCGAGGTGCTGCGCGCTGCGC 620
Db 105972 CCGGCGGGAAGGCGCTTTCGCGCGCGCCGCGCGACTGCGCGCCCGCCCGCGCG 105913
Qy 621 ACCTTCTGTCGCGCGCTGCGGCGCCAGGCGCTGCGGCGTGTGTGTCAGCGCGGAGACCGCGG 680
Db 105912 CCGCGCGCGCGCTGCGCGGCGCTTCTGCGCGCGCGCGCGCGCGCGCGCGCG 105853
Qy 681 GCTTTCGCGCGCTGTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 740
Db 105852 CCGCGCTGCTGTCGTCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 105793
Qy 741 CCGCGCGCGCGCTTCTTCCGCGAGTGGCGCTTCCCGCGGTGCGCGTCCGCGTGGGTTG 800
Db 105792 TCGCGCGCGCTGCGCGAGGAGCGGATATACAGTGTTCGCGGTGCTGCGGTG 105733
Qy 801 AGGCGCGCGCGGGAACACGCGCATGCGGAGAGCAGCGCAGCGACTCAGGCGCTTC 860
Db 105732 GCGCAGCGCTGAGTTTCTATGTC -GGGCTGTGGACCTGTGCAACCGCGTGGAGTGC 105675
Qy 861 CCGCGCAGTGTCTGCTGAGGAGTGTGTGCGCGCGCGCGCGCGCGCGCGCGCG 920
Db 105674 GCTTCTTGGCTGCTGCTGAGGAGCTTGGCGCGCAAGGACTACCACTACCTGCGCGACT 105615
Qy 921 CCGCGCGGAAGAGTGTGCGCTTTCGCGCTTTCGCGCTGTCGAGCGGCGCGCGCG 980
Db 105614 CGGAGCGCAAGGCCAACGCGCTTTCGAGACCGCGGCGCGCTGCGCGACTTCGAGAGCCG 105555
Qy 981 C 981
Db 105554 C 105554

RESULT 13

US-11-121-086-5
; Sequence 5, Application US/11121086
; Publication No. US2005026459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5
; LENGTH: 153376
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-5

Query Match 7.0%; Score 69.6; DB 7; Length 153376;

Best Local Similarity 45.5%; Pred. No. 0.0034;
Matches 322; Conservative 0; Mismatches 384; Indels 2; Gaps 2;

Qy 148 GCCCTCGTGGCGTCCCTGCAACCTTGGGAGCGCGCGCGCGCGCGCGCGCGCGCG 206
Db 56778 GTCTCTCGCAGGAGCGGTGCTTGGCGCGCGCGCGCGCGCGCGCGCGCGCG 56837
Qy 207 GCCCAGACCCCGGGTTCGCCCGGAGCAGTGTGCGTGTGCGGCGCGCGCGCGCG 266
Db 56838 GGGGAGGAGGTAACAGATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 56897
Qy 267 TGGATTCCGGGCGACAGAGCGCCAGGACCGCGCTTCCACGTGCGGAGGACTGGGGAC 326

Db 56898 GGGCGCCCGCAGTAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 56957
Qy 327 CCGGAGCACCGCTCTGCGCGCGCTTCACTTCCAGTTCGCGCTTCTTCCGCGCGAGACCCCGCC 386
Db 56958 GCGGCTTGTGATGGGCTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 57017
Qy 387 CGTCCCGACCCCTTCCCGGCTTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCG 446
Db 57018 GCGCGAGAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 57077
Qy 447 TTCTTTTCCCG 506
Db 57078 CTGCGGCTTGGCGCGCGCTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCG 57137
Qy 507 CTGCGCAGTGGGAAGCCCTTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 566
Db 57138 CCGCGAGCGGACCTGAGGCGCACTCGGCGCGCGCGCGCGCGCGCGCGCGCG 57197
Qy 567 CGAGCGTGGCTCCCTGCTGCGCAGCCTACCGGAGGTGCTGCGCGTGGCGCACGTTT 626
Db 57198 GGAAGGCGCGCGCTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 57257
Qy 627 GTGCGCGCGCTTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 685
Db 57258 GCGCGCAGTGGCGCGCGCTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 57317
Qy 686 CCGCGCGCTGTCG 745
Db 57318 CCGCGCGGAGGCGCTCCCGGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 57377
Qy 746 CGCCCGCTTCTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 805
Db 57378 AGTGGCG 57437
Qy 806 GCGCGGCGGAACCCAGCGACATGCGGAGAGCAGCGCAGCGCGACTCAGG 853
Db 57438 AGCGGTGGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 57485

RESULT 14

US-10-933-025-22/c
; Sequence 22, Application US/10933025
; Publication No. US20050265987A1
; GENERAL INFORMATION:
; APPLICANT: ROSEN, STEVEN
; APPLICANT: HEMMERICH, STEFAN
; APPLICANT: TOMITA, MEGUMI
; TITLE OF INVENTION: Sulfotransferases and methods of use
; TITLE OF INVENTION: thereof
; FILE REFERENCE: UCAL-230CON
; CURRENT APPLICATION NUMBER: US/10/933,025
; CURRENT FILING DATE: 2004-09-01
; PRIOR APPLICATION NUMBER: 10/025,966
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/258,577
; PRIOR FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: 60/267,831
; PRIOR FILING DATE: 2001-09-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 268685
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(268685)
; OTHER INFORMATION: n = A,T,C or G
US-10-933-025-22

Query Match 6.9%; Score 68.6; DB 6; Length 268685;
Best Local Similarity 48.0%; Pred. No. 0.0041;

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OM nucleic - nucleic search, using sw model

Run on: January 10, 2006, 10:37:31 ; Search time 949.333 Seconds
(without alignments)
8719.432 Million cell updates/sec

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Perfect score: 1001
Sequence: 1 cgtccgacctggagcgc.....ccccgagccttcaccacca 1001

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
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Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA Main:
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7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1001	100.0	4321	6	US-10-325-810-6
2	1001	100.0	15418	3	US-09-783-203-1
3	1001	100.0	15418	3	US-09-994-427A-1
4	1001	100.0	15418	3	US-09-995-419A-1
5	1001	100.0	15418	5	US-10-141-220-1
6	1001	100.0	15418	5	US-10-023-969-1
7	1001	100.0	15418	5	US-10-206-447-1
8	1001	100.0	15418	7	US-10-674-836-1
9	1001	100.0	15418	7	US-10-811-012-1
10	999.4	99.8	26414	8	US-10-840-455-43
11	999.4	99.8	51552	3	US-09-733-294A-30
12	945.8	94.5	4335	8	US-10-877-124-6
13	945.8	94.5	4335	8	US-10-877-022-6
14	945.8	94.5	4335	8	US-10-877-146-6
15	926.8	92.6	4200	5	US-10-044-692-6
16	926.8	92.6	4200	5	US-10-044-539-6
17	867.6	86.7	4293	8	US-10-456-830-1
18	572.2	57.2	4356	7	US-10-240-589C-144
19	546.4	54.6	5126	8	US-10-840-455-1
20	546.4	54.6	11276	8	US-10-840-455-3
21	502.2	50.2	35871	3	US-09-956-335-2
22	502.2	50.2	35978	3	US-09-956-335-1
23	499	49.9	1677	3	US-09-956-335-3

Sequence 143, Appl
Sequence 51, Appl
Sequence 55, Appl
Sequence 59, Appl
Sequence 79, Appl
Sequence 67, Appl
Sequence 83, Appl
Sequence 71, Appl
Sequence 6, Appl
Sequence 1, Appl
Sequence 2, Appl
Sequence 75, Appl
Sequence 32, Appl
Sequence 35, Appl
Sequence 93, Appl
Sequence 2, Appl
Sequence 6, Appl
Sequence 1, Appl
Sequence 2, Appl
Sequence 8, Appl
Sequence 17, Appl
Sequence 9, Appl
Sequence 8, Appl

ALIGNMENTS

RESULT 1
US-10-325-810-6
; Sequence 6, Application US/10325810
; Publication No. US20030204069A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; ; Lingner, Joachim
; ; Nakamura, Toru
; ; Chapman, Karen B.
; ; Morin, Gregg B.
; ; Harley, Calvin B.
; ; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 633
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/325,810
; FILING DATE: 20-Dec-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/402,181
; FILING DATE: 29-Sep-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951

;; FILING DATE: 14-AUG-1997
;; APPLICATION NUMBER: US 08/915,503
;; FILING DATE: 14-AUG-1997
;; APPLICATION NUMBER: WO FCT/US97/17885
;; FILING DATE: 01-OCT-1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Aussenhus, Scott L.
;; REGISTRATION NUMBER: 42,271
;; REFERENCE/DOCKET NUMBER: 015389-002620US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 576-0200
;; TELEFAX: (415) 576-0300
;; INFORMATION FOR SEQ ID NO: 6:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 4321 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; FEATURE:
;; NAME/KEY: -
;; LOCATION: 1..4321
;; OTHER INFORMATION: /note= "genomic DNA insert of pGRN144"
;; FEATURE:
;; NAME/KEY: intron
;; LOCATION: 2702..2804
;; OTHER INFORMATION: /note= "intron 1"
;; FEATURE:
;; NAME/KEY: intron
;; LOCATION: 4160..4313
;; OTHER INFORMATION: /note= "intron 2"
;; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-325-810-6

Query Match 100.0%; Score 1001; DB 6; Length 4321;
Best Local Similarity 100.0%; Pred. No. 1.2e-205;
Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CGTCCGACCTGGAGGAGCCCTGGGTCTCCGATCAGGCCAGGCGCAAGGGTCCGCG 60
Db 1938 CGTCCGACCTGGAGGAGCCCTGGGTCTCCGATCAGGCCAGGCGCAAGGGTCCGCG 1997
Qy 61 CAGCACCTGTTCCAGGGCTCCACATCATGCGCCCTCCCTGGGGTTACCCACAGCCT 120
Db 1998 CAGCACCTGTTCCAGGGCTCCACATCATGCGCCCTCCCTGGGGTTACCCACAGCCT 2057
Qy 121 AGCCCGATTGACCTCTCTCGCTGGGGCCCTCGCTGGCGCTCCCTGACACCTGGAGCGC 180
Db 2058 AGCCCGATTGACCTCTCTCGCTGGGGCCCTCGCTGGCGCTCCCTGACACCTGGAGCGC 2117
Qy 181 GAGCGGCGCGGGGGAGCGCGGCCAGACCCCGGGTCCGCCGGAGCGAGCTGGCG 240
Db 2118 GAGCGGCGCGGGGGAGCGCGGCCAGACCCCGGGTCCGCCGGAGCGAGCTGGCG 2177
Qy 241 CTGTCCGGGGCAGCGCCGGCTCCAGTGGATTCCGGGGCAGACGCCCGAGGACCGGCT 300
Db 2178 CTGTCCGGGGCAGCGCCGGCTCCAGTGGATTCCGGGGCAGACGCCCGAGGACCGGCT 2237
Qy 301 TCCACCTGGCGAGGAGCTGGGACCCCGGCGACCCGCTCTGCCCCCTTTCACCTTCCAGCT 360
Db 2238 TCCACCTGGCGAGGAGCTGGGACCCCGGCGACCCGCTCTGCCCCCTTTCACCTTCCAGCT 2297
Qy 361 CCGCTCTCTCGCGGAGACCCCGCGTCCGACCCCTCCCGGGTCCCGGGCCAGGCC 420
Db 2298 CCGCTCTCTCGCGGAGACCCCGCGTCCGACCCCTCCCGGGTCCCGGGCCAGGCC 2357
Qy 421 CTTCCGGGCTTCCAGCCCTTCCCTTCTTTCGGGGCCCGCCCTCTCTCGCGGCG 480
Db 2358 CTTCCGGGCTTCCAGCCCTTCCCTTCTTTCGGGGCCCGCCCTCTCTCGCGGCG 2417
Qy 481 CGAGTTTCAGGACAGCGTCTCTGCTGGCGACGTGGGAGCCCTGGCCCGGCGCACCC 540
Db 2418 CGAGTTTCAGGACAGCGTCTCTGCTGGCGACGTGGGAGCCCTGGCCCGGCGCACCC 2477

Qy 541 CCGGATGCGCGGCTCCCGCTCCGAGCGCTGGCTCCCTGCTGCGCAGCCACTACC 600
Db 2478 CCGGATGCGCGGCTCCCGCTCCGAGCGCTGGCTCCCTGCTGCGCAGCCACTACC 2537
Qy 601 GCGAGGTGCTGCGGCTGGCCACGTTCTGTGGGGCCCTGGGGCCCCAGGGCTGGCGGCTGG 660
Db 2538 GCGAGGTGCTGCGGCTGGCCACGTTCTGTGGGGCCCTGGGGCCCCAGGGCTGGCGGCTGG 2597
Qy 661 TGACGCGCGGGGACCCCGCGGCTTTTCGCGCGCTGTGTGGGCCCAAGTGTGCTGTGTGCTGC 720
Db 2598 TGACGCGCGGGGACCCCGCGGCTTTTCGCGCGCTGTGTGGGCCCAAGTGTGCTGTGTGCTGC 2657
Qy 721 CCTGGGAGCGACCGCGCGCCCGCGCGCCCTCTTCCGCGAGGTGGGCTCCCGGGG 780
Db 2658 CCTGGGAGCGACCGCGCGCCCGCGCGCCCTCTTCCGCGAGGTGGGCTCCCGGGG 2717
Qy 781 TCGGCGTCCGGCTGGGGTTGAGGGCGCGCCGGGGGAACAGCGACATGCGGAGAGCAGCG 840
Db 2718 TCGGCGTCCGGCTGGGGTTGAGGGCGCGCCGGGGGAACAGCGACATGCGGAGAGCAGCG 2777
Qy 841 CAGCGGACTCAGGGCTTCCCGCGAGGTGTCTGCTGCTGAAGAGTGTGTGGCCCGAGT 900
Db 2778 CAGCGGACTCAGGGCTTCCCGCGAGGTGTCTGCTGCTGAAGAGTGTGTGGCCCGAGT 2837
Qy 901 GCTGCGAGGCTGTGCGAGCGCGCGCGCGCGCCCTCTTCCGCGAGGTGGGCTTCCCGGCTGCT 960
Db 2838 GCTGCGAGGCTGTGCGAGCGCGCGCGCGCGCCCTCTTCCGCGAGGTGGGCTTCCCGGCTGCT 2897
Qy 961 GGAACGGGGCCCGGGGGCCCCCGAGGGCTTTCACCAACA 1001
Db 2898 GGAACGGGGCCCGGGGGCCCCCGAGGGCTTTCACCAACA 2938

RESULT 2

US-09-783-203-1
; Sequence 1, Application US/09783203
; Patent No. US20020098582A1
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Gold, Joseph
; APPLICANT: Lebkowski, Jane
; TITLE OF INVENTION: Tpacked stem cells
; FILE REFERENCE: 096/003
; CURRENT APPLICATION NUMBER: US/09/783,203
; CURRENT FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: 60/253,443
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/253,357
; PRIOR FILING DATE: 2000-11-27
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 15418
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-783-203-1

Query Match 100.0%; Score 1001; DB 3; Length 15418;
Best Local Similarity 100.0%; Pred. No. 8.6e-206;
Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CGTCCGACCTGGAGGAGCCCTGGGTCTCCGATCAGGCCAGGCGCAAGGGTCCGCG 60
Db 13000 CGTCCGACCTGGAGGAGCCCTGGGTCTCCGATCAGGCCAGGCGCAAGGGTCCGCG 13059
Qy 61 CAGCACCTGTTCCAGGGCTCCACATCATGCGCCCTCCCTCGGGTTACCCACAGCCT 120
Db 13060 CAGCACCTGTTCCAGGGCTCCACATCATGCGCCCTCCCTCGGGTTACCCACAGCCT 13119
Qy 121 AGCCCGATTGACCTCTCTCGCTGGGGCCCTCGCTGGCGCTTCCCTGACCCCTGGAGCGC 180
Db 13120 AGCCCGATTGACCTCTCTCGCTGGGGCCCTCGCTGGCGCTTCCCTGACCCCTGGAGCGC 13179


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QY 961 GGACGGGCGCGGGGGCCCCCCCCGAGGCTTCCACCACCA 1001
Db 13960 GGACGGGCGCGGGGGCCCCCCCCGAGGCTTCCACCACCA 14000

RESULT 4
US-09-995-419A-1
; Sequence 1, Application US/09995419A
; Publication No. US20030032187A1
; GENERAL INFORMATION:
; APPLICANT: McWhir, Jim
; APPLICANT: Geron Corporation
; APPLICANT: Schiff, J. Michael
; APPLICANT: Gold, Joseph D.
; TITLE OF INVENTION: 096,004 - SeqList
; FILE REFERENCE: 096,004 - SeqList
; CURRENT APPLICATION NUMBER: US/09/995,419A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 60/253,357
; PRIOR FILING DATE: 2000-11-27
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 15418
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-995-419A-1

Query Match 100.0%; Score 1001; DB 3; Length 15418;
Best Local Similarity 100.0%; Pred. No. 8,6e-206;
Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTCCGACCTGGAGGAGCCCTGGGTCTCCGATCAGGCGGCGCAAGGGTCCCG 60
Db 13000 CGTCCGACCTGGAGGAGCCCTGGGTCTCCGATCAGGCGGCGCAAGGGTCCCG 13059

QY 61 CAGCACCTGTCTCCAGGGCTCCACATCATATGGCCCTCCTCGGGTTACCCACAGCCT 120
Db 13060 CAGCACCTGTCTCCAGGGCTCCACATCATATGGCCCTCCTCGGGTTACCCACAGCCT 13119

QY 121 AGGCCGATTCGACCTCTCTCGCTGGGGCCCTCGCTGGCGCTCCCTGACCCCTGGAGCGC 180
Db 13120 AGGCCGATTCGACCTCTCTCGCTGGGGCCCTCGCTGGCGCTCCCTGACCCCTGGAGCGC 13179

QY 181 GAGCGGCGCGGGCGGGGAAGCGCGCCACAGACCCCGGGTCCCGCCGGAGCAGCTGCG 240
Db 13180 GAGCGGCGCGGGCGGGGAAGCGCGCCACAGACCCCGGGTCCCGCCGGAGCAGCTGCG 13239

QY 241 CTGTCCGGGGCCAGCGCGGGCTCCAGTGGATTCCGGGGCACAGACGCCAGGACCGCGCT 300
Db 13240 CTGTCCGGGGCCAGCGCGGGCTCCAGTGGATTCCGGGGCACAGACGCCAGGACCGCGCT 13299

QY 301 TCCACACCTGGCGAGGACCTGGGACCCGGGACACCCGCTCTCTGCCCCCTTCCAGCT 360
Db 13300 TCCACACCTGGCGAGGACCTGGGACCCGGGACACCCGCTCTCTGCCCCCTTCCAGCT 13359

QY 361 CGGCTCTCTCGCGCGACCCCGCCGTCCTCGACCCCTCCCGGGTCCCGGCGCCAGGCC 420
Db 13360 CGGCTCTCTCGCGCGACCCCGCCGTCCTCGACCCCTCCCGGGTCCCGGCGCCAGGCC 13419

QY 421 CCTCCGGGCTTCCAGCCCTCCCTTCTTTCGGGGCCCGCCCTCTCTCGCGCG 480
Db 13420 CCTCCGGGCTTCCAGCCCTCCCTTCTTTCGGGGCCCGCCCTCTCTCGCGCG 13479

QY 481 CGAGTTTCAGGACAGCTGTGCTCTGTGCGACGTGGGAAGCCCTGGCCCGCCAGCC 540
Db 13480 CGAGTTTCAGGACAGCTGTGCTCTGTGCGACGTGGGAAGCCCTGGCCCGCCAGCC 13539

QY 541 CCGCGATTCGCGCGCTTCCCGCTGCGAGCCGTGCGTCTGCTGCGGAGCCATACC 600
Db 13540 CCGCGATTCGCGCGCTTCCCGCTGCGAGCCGTGCGTCTGCTGCGGAGCCATACC 13599
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QY 601 GCAGAGTGTCTGCGCTGGCCACGTTGCTGCGGGCCCTGGGGCCCCAGGGCTGGCGGTGG 660
Db 13600 GCAGAGTGTCTGCGCTGGCCACGTTGCTGCGGGCCCTGGGGCCCCAGGGCTGGCGGTGG 13659

QY 661 TGCAGCGCGGGGACCCCGGGCGCTTTCCGCGCGCTGTGTGGCCAGTGTGCTGTGTGCTGC 720
Db 13660 TGCAGCGCGGGGACCCCGGGCGCTTTCCGCGCGCTGTGTGGCCAGTGTGCTGTGTGCTGC 13719

QY 721 CTTGGGACGACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 780
Db 13720 CTTGGGACGACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 13779

QY 781 TCCGCGTCCGCGCTGGGGTTCAGGGCGCGCGCGGGGGGAAACAGCGACATGCGGAGAGCAGCG 840
Db 13780 TCCGCGTCCGCGCTGGGGTTCAGGGCGCGCGGGGGGAAACAGCGACATGCGGAGAGCAGCG 13839

QY 841 CAGGCGACTCAGGGCGCTTCCCGCGAGGTGTCTGCTGAAAGAGTGTGTGGCCCCAGT 900
Db 13840 CAGGCGACTCAGGGCGCTTCCCGCGAGGTGTCTGCTGAAAGAGTGTGTGGCCCCAGT 13899

QY 901 GCTGCAGAGGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 960
Db 13900 GCTGCAGAGGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 13959

QY 961 GGACGGGCGCGCGGGGGCCCCCCCCGAGGCTTCCACCACCA 1001
Db 13960 GGACGGGCGCGCGGGGGCCCCCCCCGAGGCTTCCACCACCA 14000

RESULT 5
US-10-141-220-1
; Sequence 1, Application US/10141220
; Publication No. US20030040111A1
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Gold, Joseph
; APPLICANT: Lebkowski, Jane
; TITLE OF INVENTION: Tpacked stem cells
; FILE REFERENCE: 096/003
; CURRENT APPLICATION NUMBER: US/10/141,220
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: US/09/783,203
; PRIOR FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: 60/253,443
; PRIOR FILING DATE: 2000-11-27
; PRIOR FILING DATE: 60/253,357
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 15418
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-141-220-1

Query Match 100.0%; Score 1001; DB 5; Length 15418;
Best Local Similarity 100.0%; Pred. No. 8,6e-206;
Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTCCGACCTGGAGGAGCCCTGGGTCTCCGATCAGGCGGCGCAAGGGTCCCG 60
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QY 61 CAGCACCTGTTCAGGGGCTCCACATCATATGGCCCTCCTCGGGTTACCCACAGCCT 120
Db 13060 CAGCACCTGTTCAGGGGCTCCACATCATATGGCCCTCCTCGGGTTACCCACAGCCT 13119

QY 121 AGGCCGATTCGACCTCTCTCGCTGGGGCCCTCGCTGGCGCTCCCTGACCCCTGGAGCGC 180
Db 13120 AGGCCGATTCGACCTCTCTCGCTGGGGCCCTCGCTGGCGCTCCCTGACCCCTGGAGCGC 13179

QY 181 GAGCGGCGCGGGCGGGGAAGCGCGCCACAGACCCCGGGTCCCGCCGGAGCAGCTGCG 240
Db 13180 GAGCGGCGCGGGCGGGGAAGCGCGCCACAGACCCCGGGTCCCGCCGGAGCAGCTGCG 13239

QY 241 CTGTCCGGGGCCAGCGCGGGCTCCAGTGGATTCCGGGGCACAGACGCCAGGACCGCGCT 300
Db 13240 CTGTCCGGGGCCAGCGCGGGCTCCAGTGGATTCCGGGGCACAGACGCCAGGACCGCGCT 13299

QY 301 TCCACACCTGGCGAGGACCTGGGACCCGGGACACCCGCTCTCTGCCCCCTTCCAGCT 360
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QY 361 CGGCTCTCTCGCGCGACCCCGCCGTCCTCGACCCCTCCCGGGTCCCGGCGCCAGGCC 420
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QY 421 CCTCCGGGCTTCCAGCCCTCCCTTCTTTCGGGGCCCGCCCTCTCTCGCGCG 480
Db 13420 CCTCCGGGCTTCCAGCCCTCCCTTCTTTCGGGGCCCGCCCTCTCTCGCGCG 13479

QY 481 CGAGTTTCAGGACAGCTGTGCTCTGTGCGACGTGGGAAGCCCTGGCCCGCCAGCC 540
Db 13480 CGAGTTTCAGGACAGCTGTGCTCTGTGCGACGTGGGAAGCCCTGGCCCGCCAGCC 13539

QY 541 CCGCGATTCGCGCGCTTCCCGCTGCGAGCCGTGCGTCTGCTGCGGAGCCATACC 600
Db 13540 CCGCGATTCGCGCGCTTCCCGCTGCGAGCCGTGCGTCTGCTGCGGAGCCATACC 13599
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; Sequence 1, Application US/10206447			
; Publication No. US20030095616A1			
; GENERAL INFORMATION:			
; APPLICANT: Geron Corporation			
; APPLICANT: Irving, John			
; APPLICANT: Karpf, David			
; APPLICANT: Schiff, Michael			
; TITLE OF INVENTION: DUAL SPECIFICITY TUMOR KILLING VECTORS DRIVEN BY THE TELOMERASE H			
; FILE REFERENCE: 085/002			
; CURRENT APPLICATION NUMBER: US/10/206,447			
; PRIOR FILING DATE: 2002-07-25			
; PRIOR APPLICATION NUMBER: 60/308,029			
; PRIOR FILING DATE: 2001-07-25			
; NUMBER OF SEQ ID NOS: 2			
; SOFTWARE: PatentIn version 3.1			
; SEQ ID NO 1			
; LENGTH: 15418			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-10-206-447-1			
Query Match 100.0%; Score 1001; DB 5; Length 15418;			
Best Local Similarity 100.0%; Pred. No. 8.6e-206;			
Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1	CGTCCGACCTGGAGGCGAGCCCTGGGTCTCCGGATCAGGCGGCGGCAAGGGTGC	60
Db	13000	CGTCCGACCTGGAGGCGAGCCCTGGGTCTCCGGATCAGGCGGCGGCAAGGGTGC	13059
Qy	61	CACGACCTGTTCACAGGCGCTCCACATCATATGCGCCCTCCCTCGGGTTACCCACAGCCT	120
Db	13060	CACGACCTGTTCACAGGCGCTCCACATCATATGCGCCCTCCCTCGGGTTACCCACAGCCT	13119
Qy	121	AGGCGGATTCGACCTCTCTCGCTGGGGCCCTCGCTGGGGTTCCTGACCTGGGAGCGC	180
Db	13120	AGGCGGATTCGACCTCTCTCGCTGGGGCCCTCGCTGGGGTTCCTGACCTGGGAGCGC	13179
Qy	181	GAGCGGCGCGGGGAGCGCGCCAGAGCCCGGGTCCCGGTCGCGGAGCAGCTGCG	240
Db	13180	GAGCGGCGCGGGGAGCGCGCCAGAGCCCGGGTCCCGGTCGCGGAGCAGCTGCG	13239
Qy	241	CTGTCCGGGCGCAGGCGCGGCTCCAGTGATTCGCGGCGACAGACGCCCGAGCGCGCT	300
Db	13240	CTGTCCGGGCGCAGGCGCGGCTCCAGTGATTCGCGGCGACAGACGCCCGAGCGCGCT	13299
Qy	301	TCCACGCTGGCGAGGAGCTGGGACCGCGGCGACCGCGTCTGTGCGCCCTTACCTTCCAGCT	360
Db	13300	TCCACGCTGGCGAGGAGCTGGGACCGCGGCGACCGCGTCTGTGCGCCCTTACCTTCCAGCT	13359
Qy	361	CCGCTCTCTCGCGGAGACCCCGCGCTCCGACCCCTCCCGGTCCCGGCGCCAGGCC	420
Db	13360	CCGCTCTCTCGCGGAGACCCCGCGCTCCGACCCCTCCCGGTCCCGGCGCCAGGCC	13419
Qy	421	CCTCGGCGCCCTCCAGCCCTCCCTTCTTCCTGCGGCGCCCGCCCTCTCTCTCGCGCG	480
Db	13420	CCTCGGCGCCCTCCAGCCCTCCCTTCTTCCTGCGGCGCCCGCCCTCTCTCTCGCGCG	13479
Qy	481	CGATTTTCAGCAGCGCTGCTGTGTGCGACAGTGGGAAGCCCTGGCCCGGCGCACCC	540
Db	13480	CGATTTTCAGCAGCGCTGCTGTGTGCGACAGTGGGAAGCCCTGGCCCGGCGCACCC	13539
Qy	541	CCGCGATGCGCGCGCTCCCGCTGCGAGCGCTCCCTCTCTGCGGAGCCACTACC	600
Db	13540	CCGCGATGCGCGCGCTCCCGCTGCGAGCGCTCCCTCTCTGCGGAGCCACTACC	13599
Qy	601	GCGAGGTGCTCCGCTGCGCACGTTCTGTGCGGCGCTTGGGCGCCCGAGGGCTGGCGGTGG	660
Db	13180	GAGCGGCGCGGGGAGCGCGCCAGAGCCCGGGTCCCGGTCGCGGAGCAGCTGCG	13239
RESULT 8			
US-10-674-836-1			
; Sequence 1, Application US/10674836			
; Publication No. US2004007287A1			
; GENERAL INFORMATION:			
; APPLICANT: Morin, Gregg B. Serge			
; APPLICANT: Lichtsteiner, Alain			
; APPLICANT: Vasserot, Alain			
; APPLICANT: Adams, Robert R.			
; APPLICANT: Geron Corporation			
; TITLE OF INVENTION: Telomerase Reverse Transcriptase Transcriptional			
; FILE REFERENCE: 019/246P			
; CURRENT APPLICATION NUMBER: US/10/674,836			
; CURRENT FILING DATE: 2003-09-29			
; PRIOR APPLICATION NUMBER: US/09/244,438			
; PRIOR FILING DATE: 1999-02-04			
; NUMBER OF SEQ ID NOS: 23			
; SOFTWARE: PatentIn Ver. 2.1			
; SEQ ID NO 1			
; LENGTH: 15418			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
; FEATURE:			
; OTHER INFORMATION: Human TERT promoter			
US-10-674-836-1			
Query Match 100.0%; Score 1001; DB 7; Length 15418;			
Best Local Similarity 100.0%; Pred. No. 8.6e-206;			
Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1	CGTCCGACCTGGAGGCGAGCCCTGGGTCTCCGGATCAGGCGGCGGCAAGGGTGC	60
Db	13000	CGTCCGACCTGGAGGCGAGCCCTGGGTCTCCGGATCAGGCGGCGGCAAGGGTGC	13059
Qy	61	CACGACCTGTTCACAGGCGCTCCACATCATATGCGCCCTCCCTCGGGTTACCCACAGCCT	120
Db	13060	CACGACCTGTTCACAGGCGCTCCACATCATATGCGCCCTCCCTCGGGTTACCCACAGCCT	13119
Qy	121	AGGCGGATTCGACCTCTCTCGCTGGGGCCCTCGCTGGGGTTCCTGACCTGGGAGCGC	180
Db	13120	AGGCGGATTCGACCTCTCTCGCTGGGGCCCTCGCTGGGGTTCCTGACCTGGGAGCGC	13179
Qy	181	GAGCGGCGCGGGGAGCGCGCCAGAGCCCGGGTCCCGGTCGCGGAGCAGCTGCG	240
Db	13180	GAGCGGCGCGGGGAGCGCGCCAGAGCCCGGGTCCCGGTCGCGGAGCAGCTGCG	13239
Qy	241	CTGTCCGGGCGCAGGCGCGGCTCCAGTGATTCGCGGCGACAGACGCCCGAGCGCGCT	300
Db	13240	CTGTCCGGGCGCAGGCGCGGCTCCAGTGATTCGCGGCGACAGACGCCCGAGCGCGCT	13299
Qy	301	TCCACGCTGGCGAGGAGCTGGGACCGCGGCGACCGCGTCTGTGCGCCCTTACCTTCCAGCT	360
Db	13300	TCCACGCTGGCGAGGAGCTGGGACCGCGGCGACCGCGTCTGTGCGCCCTTACCTTCCAGCT	13359
Qy	361	CCGCTCTCTCGCGGAGACCCCGCGCTCCGACCCCTCCCGGTCCCGGCGCCAGGCC	420
Db	13360	CCGCTCTCTCGCGGAGACCCCGCGCTCCGACCCCTCCCGGTCCCGGCGCCAGGCC	13419
Qy	421	CCTCGGCGCCCTCCAGCCCTCCCTTCTTCCTGCGGCGCCCGCCCTCTCTCTCGCGCG	480
Db	13420	CCTCGGCGCCCTCCAGCCCTCCCTTCTTCCTGCGGCGCCCGCCCTCTCTCTCGCGCG	13479
Qy	481	CGATTTTCAGCAGCGCTGCTGTGTGCGACAGTGGGAAGCCCTGGCCCGGCGCACCC	540
Db	13480	CGATTTTCAGCAGCGCTGCTGTGTGCGACAGTGGGAAGCCCTGGCCCGGCGCACCC	13539
Qy	541	CCGCGATGCGCGCGCTCCCGCTGCGAGCGCTCCCTCTCTGCGGAGCCACTACC	600
Db	13540	CCGCGATGCGCGCGCTCCCGCTGCGAGCGCTCCCTCTCTGCGGAGCCACTACC	13599
Qy	601	GCGAGGTGCTCCGCTGCGCACGTTCTGTGCGGCGCTTGGGCGCCCGAGGGCTGGCGGTGG	660

241 CTGTCGGGGCCAGGCGCGGCTCCAGTGGATTTCGCGGCAACAGACGCCAGGACCGCGCT 300
Db |||||
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301 TCCACAGTGGCGGAGGAGCTGGGACCCGCGCAACCGCTCTGCGCCCTTCACTTCCAGCT 360
Db |||||
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Qy |||||
361 CCGGCTCTCTCGCGGAGACCCGCGCGGCTCCGAGACCTTCCCGGCTCCCGGCGCAGCC 420
Db |||||
13360 CCGGCTCTCTCGCGGAGACCCGCGCGGCTCCGAGACCTTCCCGGCTCCCGGCGCAGCC 13419
Qy |||||
421 CTTCCGGGCTCTCCAGGCGCTCCCTCTCTCTTTCGCGGCGCCCGCTCTCTCTCGCGG 480
Db |||||
13420 CTTCCGGGCTCTCCAGGCGCTCCCTCTCTCTTTCGCGGCGCCCGCTCTCTCTCGCGG 13479
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481 CGAGTTTTCAGGACGCTGCT 540
Db |||||
13480 CGAGTTTTCAGGACGCTGCT 13539
Qy |||||
541 CCGGATGTCGCGGCGCTCCCGCT 600
Db |||||
13540 CCGGATGTCGCGGCGCTCCCGCT 13599
Qy |||||
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13600 GCGAGTGTCTGCGGCT 13659
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13780 TCGGCTCTCGGCTGAGGCG 13839
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901 GCTGAGAGGCTGTGCGAGCG 960
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US-10-811-012-1
; Sequence 1, Application US/10811012
; Publication No. US20040152189A1
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: McWhir, Jim
; APPLICANT: Gold, Joseph D.
; APPLICANT: Schiff, J. Michael
; TITLE OF INVENTION: Selective Antibody Targeting of Undifferentiated Stem Cells
; FILE REFERENCE: 096,06D- Seglist
; CURRENT APPLICATION NUMBER: US/10/811,012
; CURRENT FILING DATE: 2004-03-26
; PRIOR APPLICATION NUMBER: 09/995,419
; PRIOR FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 60/253,357
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/253,443
; PRIOR FILING DATE: 2000-11-27

; PRIOR APPLICATION NUMBER: 60/253,395
; PRIOR FILING DATE: 2000-11-27
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 15418
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-811-012-1

Query Match 100.0%; Score 1001; DB 7; Length 15418;
Best Local Similarity 100.0%; Pred. No. 8.6e-206;
Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 13000 CGTCCGACCTGAGGAGCAGCCCTGGGCTCTCCGATCAGGCGCAGGCGCCCAAGGGTTCGCG 13059
Qy 61 CACGCACTGTTCACAGGCGCTCCACATCATATGAGCCCTCTCTCTCGGGTTACCCACAGCT 120
Db 13060 CACGCACTGTTCACAGGCGCTCCACATCATATGAGCCCTCTCTCTCGGGTTACCCACAGCT 13119
Qy 121 AGGCGGATTCGACCTCTCTCTCGGCTGGGGCCCTCTCTGCGTCCCTGACACCTTGGAGCGC 180
Db 13120 AGGCGGATTCGACCTCTCTCTCGGCTGGGGCCCTCTCTGCGTCCCTGACACCTTGGAGCGC 13179
Qy 181 GAGCGGCGCGCGGCGGAGAGCGCGCCACAGACCCCGGCTCCCGCGGAGCAGCTGCG 240
Db 13180 GAGCGGCGCGCGGCGGAGAGCGCGCCACAGACCCCGGCTCCCGCGGAGCAGCTGCG 13239
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Qy 301 TCCACAGTGGCGGAGGAGCTGGGACCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
Db 13300 TCCACAGTGGCGGAGGAGCTGGGACCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 13359
Qy 361 CCGGCTCTCTCGCGGAGACCCG 420
Db 13360 CCGGCTCTCTCGCGGAGACCCG 13419
Qy 421 CTTCCGGGCGCTTCCAGCCT 480
Db 13420 CTTCCGGGCGCTTCCAGCCT 13479
Qy 481 CAGTGTTCAGGAGCGCTGCGCT 540
Db 13480 CAGTGTTCAGGAGCGCTGCGCT 13539
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Qy 601 GCGAGTGTCTGCGGCT 660
Db 13600 GCGAGTGTCTGCGGCT 13659
Qy 661 TGCAGCGCGGAGACCCGCGGCGCTTTCGCGGCGCCCGCTCTCTCTCTCTCTCTCTCTCTCTCT 720
Db 13660 TGCAGCGCGGAGACCCGCGGCGCTTTCGCGGCGCCCGCTCTCTCTCTCTCTCTCTCTCTCTCT 13719
Qy 721 CTTGAGCGCGGAGACCCGCGGCGCTTTCGCGGCGCCCGCTCTCTCTCTCTCTCTCTCTCTCTCT 780
Db 13720 CTTGAGCGCGGAGACCCGCGGCGCTTTCGCGGCGCCCGCTCTCTCTCTCTCTCTCTCTCTCTCT 13779
Qy 781 TCGGCTCTCGGCTGAGGCG 840
Db 13780 TCGGCTCTCGGCTGAGGCG 13839
Qy 841 CAGGCGACTCAGGCGCGCTTCCCG 900
Db 13840 CAGGCGACTCAGGCGCGCTTCCCG 13899

OTHER INFORMATION: exon 3
NAME/KEY: intron
LOCATION: (21763)...(23851)
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NAME/KEY: exon
LOCATION: (23852)...(24032)
OTHER INFORMATION: exon 4
NAME/KEY: intron
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NAME/KEY: exon
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NAME/KEY: intron
LOCATION: (47174)...(47709)
OTHER INFORMATION: intron 15
NAME/KEY: exon
LOCATION: (47710)...(50544)
OTHER INFORMATION: exon 16
US-09-733-294A-30
Query Match 99.8%; Score 999.4; DB 3; Length 51552;
Best Local Similarity 99.9%; Pred. No. 1.4e-205;
Matches 1000; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 10789 CACGCACCTGTTCACAGGGCTCCACATCATATGGGCCCTCCCTCGGGTTACCCACAGCCT 10848
Qy 121 AGGCCGATTGACCTCTCTCGCTGGGCTCTCGTGGCTCTCTGCACTCCCTGGAGGCGC 180
Db 10849 AGGCCGATTGACCTCTCTCGCTGGGCTCTCGTGGCTCTCTGCACTCCCTGGAGGCGC 10908
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Qy 241 CTGTCCGGGCGAGGCCCGGGCTCCAGTGGATTTCGGGGCACAGACGCCCAGGACCGCGCT 300
Db 10969 CTGTCCGGGCGAGGCCCGGGCTCCAGTGGATTTCGGGGCACAGACGCCCAGGACCGCGCT 11028
Qy 301 TCCACGTTGCGGAGGAGCTGGGGACCGGGGACCCGCTCTGCGCCCTTTCACTTCAGCT 360
Db 11029 CCCCACGTGGCGGAGGAGCTGGGGACCGGGGACCCGCTCTGCGCCCTTTCACTTCAGCT 11088
Qy 361 CCGCTCTCTCGCGGGACCCCGGCTCCCGACCCCTCCCGGGTCCCGGCCAGGCC 420
Db 11089 CCGCTCTCTCGCGGGACCCCGGCTCCCGACCCCTCCCGGGTCCCGGCCAGGCC 11148
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Db 11149 CCTCGGGCTCTCCAGCCCTCTCCCTCTCTTTCGGGGCCCGCCCTCTCTCGCGGG 11208
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Db 11269 CCGGATGCCCGGGCTCCCGCTGCGAGCGCTGCTCCCTGCTGGCGAGCACTACC 11328
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Db 11329 GCGAGTGTCTCGCTGSCACGTTCTGTCGCGCTGCGGGCCCGAGGCTGGCGGCTGG 11388
Qy 661 TGCAGCGCGGGACCCCGCGGCTTTTCGCGGCTGCTGGTCCCGAGTGTCTGCTGTC 720
Db 11389 TGCAGCGCGGGACCCCGCGGCTTTTCGCGGCTGCTGGTCCCGAGTGTCTGCTGTC 11448
Qy 721 CCTGGGACGCAAGCGCGGCCCGCGCTGCTGCGAGCGCTGCTCCCTGCTGGCGAGTCC 780
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Qy 781 TCGCGTCCGCTGGGTTGAGGGCGCGCGGGGAAACAGGACATCGGAGAGCAGCG 840
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Qy 841 CAGCGACTCAGGGCGCTTCCCGCGAGTGTCTGCTGAGGAGCTGGTGGCCCGAGT 900


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Qy 597 TACCGCAGGTGCTGCGCTGGCCACAGTCTGTGGGCGCCTGGGGCCCGCAGGGCTGGCGG 656
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Qy 2547 TACCGCAGGTGCTGCGCTGGCCACAGTCTGTGGGCGCCTGGGGCCCGCAGGGCTGGCGG 2606
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Qy 657 CTGCTGACGCGCGGGACCGCGGCTTTTCGCGCGCTGTGTGGCCCAAGTGCCTGGTGTGC 716
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Qy 2607 CTGCTGACGCGCGGGACCGCGGCTTTTCGCGCGCTGTGTGGCCCAAGTGCCTGGTGTGC 2666
Db |||||
Qy 717 GTGCTGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 776
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Qy 2667 GTGCTGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2726
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Qy 777 GGGGTGCGCGCTGCGCTGGGGTTCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 836
Db |||||
Qy 2727 GGGGTGCGCGCTGCGCTGGGGTTCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2786
Db |||||
Qy 837 AGCGCAGCGCACTCAGGCGCGCTTCCCGCGCAGGTGTCTGCTGGAAGGAGCTGGTGGCCC 896
Db |||||
Qy 2787 AGCGCAGCGCACTCAGGCGCGCTTCCCGCGCAGGTGTCTGCTGGAAGGAGCTGGTGGCCC 2846
Db |||||
Qy 897 GAGTGTGACAGAGCTGTGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 956
Db |||||
Qy 2847 GAGTGTGACAGAGCTGTGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2906
Db |||||
Qy 957 TGCTGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1001
Db |||||
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Db |||||
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RESULT 14

US-10-877-146-6

; Sequence 6, Application US/10877146

; Publication No. US20050013825A1

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.

Lingner, Joachim

Nakamura, Toru

Chapman, Karen B.

Morin, Gregg B.

Harley, Calvin B.

Andrews, William H.

TITLE OF INVENTION: Human Telomerase Catalytic Subunit

NUMBER OF SEQUENCES: 727

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/877,146

FILING DATE: 24-Jun-2004

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/432,503

FILING DATE: 02-Nov-1999

APPLICATION NUMBER: 08/974,549

FILING DATE: <Unknown>

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997

APPLICATION NUMBER: US 08/851,843

FILING DATE: 06-MAY-1997

APPLICATION NUMBER: US 08/854,050

FILING DATE: 09-MAY-1997

APPLICATION NUMBER: US 08/911,312

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;
;
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4335 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..4335
; OTHER INFORMATION: /note= "genomic DNA insert of pGRN144"
;
;
; NAME/KEY: intron
; LOCATION: 2715..2818
; OTHER INFORMATION: /note= "intron 1"
;
;
; NAME/KEY: intron
; LOCATION: 4173..4326
; OTHER INFORMATION: /note= "intron 2"
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-877-146-6
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Query Match 94.5%; Score 945.8; DB 8; Length 4335;

Best Local Similarity 98.9%; Pred. No. 8e-194;

Matches 994; Conservative 0; Mismatches 7; Indels 4; Gaps 4;

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Qy 1 CGTCCGACCTGGAGGCGAGCCCTGGGGTCTCCGATCAGGCGAGCGCGGCAAGGGTCCGCG 60
Db 1947 CGTCCGACCTGGAGGCGAGCCCTGGGGTCTCCGATCAGGCGAGCGCGGCAAGGGTCCGCG 2006
Qy 61 CACGCACTGTTCCTCCAGGGCTCCACATCATATGCCCCCTCCCTCGGGTTACCCACAGCCT 120
Db 2007 CACGCACTGTTCCTCCAGGGCTCCACATCATATGCCCCCTCCCTCGGGTTACCCACAGCCT 2066
Qy 121 AGGCGGATTGACCTCTTCGCTGGGGCCCTCGCTGGCGTCCCTGACACCTGGGAGCGC 180
Db 2067 AGGCGGATTGACCTCTTCGCTGGGGCCCTCGCTGGCGTCCCTGACACCTGGGAGCGC 2126
Qy 181 GAGCGGCGCGCGCGGGAAGCGCGCCAGACCCCGGGTCCGCGCGAGCAGCTGCG 240
Db 2127 GAGCGGCGCGCGCGGGAAGCGCGCCAGACCCCGGGTCCGCGCGAGCAGCTGCG 2186
Qy 241 CTGTCCGGGCGCAGCGCGGGCTCCCACTGAGTTCGCGGGC-ACAGACGCCAGGACCGCGC 299
Db 2187 CTGTCCGGGCGCAGCGCGGGCTCCCACTGAGTTCGCGGGCAACAGACGCCAGGACCGCGC 2246
Qy 300 TTCCACAGTGGCGGAGGACTGGGAGCCCGGGACCCCGTCTGCGCCCTTACCTTCAGC 359
Db 2247 TTCCACAGTGGCGGAGGACTGGGAGCCCGGGACCCCGTCTGCGCCCTTACCTTCAGC 2306
Qy 360 TCCGCTCTCTTCGCGGG-ACCCCGCGCGTCCCG-ACCCCTCCCGGGTCCCGGCCCGCAG 417
Db 2307 TCCGCTCTCTTCGCGGGAAACCCCGCCCTTCCGAAACCTTCCCGGGTCCCGGCCCGCAG 2366
Qy 418 CCCCCTCCGGGCGCTCCAGCCCTCCCTTCC-TTTTCCGGCGGCCCGCGCTCTCTCGC 476
Db 2367 CCCCCTCCGGGCGCTCCAGCCCTCCCTTCCCTTTTCCGGCGGCCCGCGCTCTCTCGC 2426
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Qy	477	GGCGCGAGTTTCAGGCGAGCGCTCGCTCTGCTCGCGACGTGGGAAGCCCTGGCCCCCGGC	536
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Qy	537	ACCCCGCGATGCGCGCGCTCCCGCTGCCGAGCGGTGCGCTCCCTGCTGCGCAGCCAC	596
Db	2487	ACCCCGCGATGCGCGCGCTCCCGCTGCCGAGCGGTGCGCTCCCTGCTGCGCAGCCAC	2546
Qy	597	TACCGGAGTGTGCGCTGGGCCAGTTCTGTGCGGCGCTGGGGCCCCAGGGCTGGCG	656
Db	2547	TACCGGAGTGTGCGCTGGGCCAGTTCTGTGCGGCGCTGGGGCCCCAGGGCTGGCG	2606
Qy	657	CTGGTGACGCGCGGGGACCCGGCGGCTTTTCGGCGCGCTGGTGCGGCCACAGTGCCTGGTGTC	716
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Qy	777	GGGTCTGGGCTTCGGCTTGGGGTTGAGGGCGGGCGGGGGGAAACAGCGACATGCGGAGAGC	836
Db	2727	GGGTCTGGGCTTCGGCTTGGGGTTGAGGGCGGGCGGGGGGAAACAGCGACATGCGGAGAGC	2786
Qy	837	AGCGCAGGCACTCAGGGCGCTTCCCCCGCAGGTGTCCTGCTTGAGGAGCTGGTGGCCC	896
Db	2787	AGCGCAGGCACTCAGGGCGCTTCCCCCGCAGGTGTCCTGCTTGAGGAGCTGGTGGCCC	2846
Qy	897	GAGTGTCTCAGAGGCTGTGCGAGCGCGCGCGGAAGAACGTGCTGGGCTTCGGGCTTCGCGC	956
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Qy	957	TGCTGGACGGGGCCCCCGGGGGCCCCCCCCCGAGGCGCTTTCACACCA	1001
Db	2907	TGCTGGACGGGGCCCCCGGGGGCCCCCCCCCGAGGCGCTTTCACACCA	2951

RESULT 15

US-10-044-692-6

US-10-011-024-0
: Sequence 6. Application US/10044692

; sequence 8; Application No: US20030096344A1

GENERAL INFORMATION:

APPLICANT: Czech
Thomas R

APPLICANT: Cech, Thomas R.
Linmer, Joseph

Lingner, Joachi
Nakamura Toti

;
;
;
Nakamura, Toru
Cherman, Kazuo P

Chapman, Karen
Morrin, Craig D

1. Morin, Gregg B.

Harley, Calvin

Andrews, William H.

; TITLE OF INVENTION: HUMAN TELOMERASE CA

THE

; NUMBER OF SEQUENCES: 335

CORRESPONDENCE ADDRESS:

ADDRESSES: Townsend and Townsend and Crew

STREET: Two Embarca

CITY: San Francisco

STATE: California

COUNTRY: U

ZIP: 94111

COMPUTER READABLE FORM:

```

/
;
MEDIUM TYPE: Floppy disk

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COMPUTER: IBM PC compatible

COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS

OPERATING SYSTEM: PC
SOFTWARE: PatentIn 8

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; : SOFTWARE: PACENTLIN Release #1.0,
; : CURRENT APPLICATION DATA:

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; CURRENT APPLICATION DATA: IT
 . APPLICATION NUMBER: IT
 .

APPLICATION NUMBER: US/10
FILING DATE: 11-Jan-2002

FILING DATE: 11-JAN-80
CLASSIFICATION: UNCLASSIFIED

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;
;
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA.

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PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/912,951

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Qy      656  GCTGGTCAGCGCGGGACCCGCGGCTTTCCGCGCTGTGTGCCAGTGCCCTGGTGTG  715
Db      2423  GCTGGTCAGCGCGGGACCCGCGGCTTTCCGCGCTGTGTGCCAGTGCCCTGGTGTG  2482
Qy      716  CGTCCCTTGGGACGCA CGGCGCCCCCGCGCCCCCTCTCTTCGCGCAGGTGGGCTTCCC  775
Db      2483  CGTCCCTTGGGACGCA CGGCGCCCCCGCGCCCCCTCTCTTCGCGCAGGTGGGCTTCCC  2542
Qy      776  CGGGGTCGGCGTCCGGCTGGGGTTGAGGGCGGCCCGGGGGAACGAGGACATGCGGAGAG  835
Db      2543  CGGGGTCGGCGTCCGGCTGGGGTTGAGGGCGGCCCGGGGGAACGAGGACATGCGGAGAG  2602
Qy      836  CAGCGCAGGCGACTCAGGGCGCTTCCCGCGCAGGTGTCTTGCCTGAAGGAGCTGTGGGCC  895
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Qy      896  CGAGTGTCTCAGAGGCTGTGCGAGCGCGCGCGGAAGAACGTGTGGCTTTCGGCTTCGCG  955
Db      2663  CGAGTGTCTCAGAGGCTGTGCGAGCGCGCGCGGAAGAACGTGTGGCTTTCGGCTTCGCG  2722
Qy      956  CTGCTGACCGGGGCCCGGGGGCCCCCGAGGCTTCACCA  1001
Db      2723  CTGCTGACCGGGGCCCGGGGGCCCCCGAGGCTTCACCA  2768
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Search completed: January 10, 2006, 20:35:13
Job time : 951.333 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 10, 2006, 05:46:59 ; Search time 690.667 Seconds
(without alignments)
9659.301 Million cell updates/sec

Title: US-09-615-039-1_COPY_13000_14000

Perfect score: 1001

Sequence: 1 cgtccgacctggagcgc.....ccccgagcgttcaccacca 1001

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N Geneseq 21.*

- 1: geneseqn1980s.*
- 2: geneseqn1990s.*
- 3: geneseqn2000s.*
- 4: geneseqn2001as.*
- 5: geneseqn2001bs.*
- 6: geneseqn2002as.*
- 7: geneseqn2002bs.*
- 8: geneseqn2003as.*
- 9: geneseqn2003bs.*
- 10: geneseqn2003cs.*
- 11: geneseqn2003ds.*
- 12: geneseqn2004as.*
- 13: geneseqn2004bs.*
- 14: geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	1001	100.0	2501	14 ADV97952	Adv97952 Human tum
C 2	1001	100.0	7928	14 AEA18047	Aea18047 Human gyn
C 3	1001	100.0	15418	3 AEA63785	Aea63785 Nucleotid
4	1001	100.0	15418	6 AAL38601	Aal38601 Human TER
5	1001	100.0	15418	6 ABS54997	Ab54997 Lambda cl
6	1001	100.0	15418	6 AAL38595	Aal38595 DNA of pl
7	1001	100.0	15418	10 ADC21253	Adc21253 Lambda cl
8	999.4	99.8	5491	13 ADU82631	Adu82631 Human hTE
9	999.4	99.8	51552	6 AAS96607	Aas96607 DNA encod
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C 14	629.8	62.9	2501	14 ADV98042	Adv98042 Bisulfite
C 15	629.8	62.9	7928	14 AEA18046	Aea18046 Converted
C 16	582	58.1	3962	4 AAL41091	Aal41091 Telomeras
C 17	572.2	57.2	4356	6 ABL92335	Ab192335 Chemical
C 18	546.4	54.6	5126	2 AAX88272	Aax88272 Human cat
C 19	521.4	52.1	2501	14 ADV98043	Adv98043 Bisulfite

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C 21	502.2	50.2	35871	6	AAD27972	Aad27972 Recombina
C 22	502.2	50.2	35978	6	AAD27971	Aad27971 Recombina
C 23	499	49.9	1677	6	AAD27973	Aad27973 Human tel
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25	456	45.6	3500	2	AAX18275	Axi18275 Telomeras
26	455	45.5	3543	8	ABZ69628	Abz69628 Plasmid c
C 27	453.4	45.3	455	12	ADI33422	Adi33422 Human tel
C 28	442.6	44.2	2501	14	ADV98136	Adv98136 Bisulfite
C 29	442.6	44.2	7928	14	AEA18066	Aea18066 Converted
C 30	412.4	41.2	495	13	ADT77582	Adt77582 hTERT min
C 31	412.4	41.2	8565	13	ADT77585	Adt77585 TSTA-hTER
32	411	41.1	902	13	ADR73427	Adr73427 Human m-h
33	408	40.8	408	13	ADR73423	Adr73423 Human tel
34	397	39.7	397	6	ABS98658	Ab598658 Human TER
C 35	397	39.7	397	14	ADZ08730	Adz08730 Human TER
C 36	390.4	39.0	460	14	ADV23870	Adv23870 Human hTE
37	389.6	38.9	454	11	ADN00285	Adn00285 Tumour-sp
38	376.4	37.6	378	8	ACC47272	Acc47272 CEA gene
39	334.8	33.4	2501	14	ADV98137	Adv98137 Bisulfite
C 40	334.8	33.4	7928	14	AEA18067	Aea18067 Converted
C 41	329.6	32.9	1404	6	AAD22344	Aad22344 Chemical
42	324	32.4	324	13	ADW76702	Adw76702 DNA relat
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45	298.2	29.8	314	3	AAA94134	Aaa94134 Telomeras

ALIGNMENTS

RESULT 1

ADV97952/c

ID ADV97952 standard; DNA; 2501 BP.

XX

AC ADV97952;

XX

DT 10-MAR-2005 (first entry)

XX

DE Human tumor-associated cancer-testis antigen tert DNA Seq 44.

XX

ds; immunotherapy; DNA methylation; tumor-associated antigen; cancer; cytostatic; vaccine; tert.

XX

OS Homo sapiens.

XX

PN EPI491639-A2.

XX

PD 29-DEC-2004.

XX

PF 17-JUN-2004; 2004EP-00090238.

XX

PR 24-JUN-2003; 2003DE-01029240.

XX

PA (EPIG-) EPIGENOMICS AG.

XX

PI Eichler-Mertens M, Piepenbrock C, Olek A;

XX

DR WPI; 2005-050366/06.

XX

PT Identifying target points for immunotherapy of tumors by analysis of methylation status of many tumor-associated antigens, also treatment, particularly vaccination, using selected antigens.

XX

PS Disclosure; SEQ ID NO 44; 206pp; German.

XX

CC This invention relates to a novel method for determining target points for tumor immunotherapy by taking a DNA sample from serum or other bodily fluids of a patient. Specifically, it refers to identifying the methylation status of at least one CpG island in each of 47 identified tumor-associated antigens in order to generate a methylation pattern from the results. It describes an analysis of methylation status that includes chemical treatment of DNA with a bisulfite, optionally followed by

CC amplification, particularly methylation specific PCR (MSP) and/or a
CC heavy methyl technique. Accordingly, the present invention provides tumor
CC associated antigen sequences and also the corresponding bisulfite
CC sequences generated under differing methylation conditions. As such, the
CC method can be used to identify targets for immunotherapy of cancers,
CC specifically by vaccination against selected tumor-associated antigens to
CC provide individualized immunotherapy. Furthermore, the method allows
CC simultaneous determination of methylation status of many tumor antigens
CC and also of other methylation-regulated cofactors important for
CC vaccination. The pharmaceutical compositions derived thereof exhibit
CC cytotoxic activity and can be used in the development of vaccines. This
CC polynucleotide sequence is a human tumor associated cancer-testis antigen
CC DNA sequence of the invention.

XX SQ Sequence 2501 BP; 504 A; 767 C; 827 G; 403 T; 0 U; 0 Other;

Query Match 100.0%; Score 1001; DB 14; Length 2501;
Best Local Similarity 100.0%; Pred. No. 8.1e-138;
Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTCCGACCTGGAGGAGCCCTGGGTCTCGGATCAGGCAGCGGCAAAAGGTCCCG 60
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QY 61 CACGACCTGTTCCAGGGCTCCACATCATGCGCCCTCCTCGGGTTACCCACAGCCT 120
DB 986 CACGACCTGTTCCAGGGCTCCACATCATGCGCCCTCCTCGGGTTACCCACAGCCT 927
QY 121 AGCCCGATTGACCTCTCTCGCTGGGGCCCTCGCTGCGCTGCTGACCCCTGGAGCGC 180
DB 926 AGCCCGATTGACCTCTCTCGCTGGGGCCCTCGCTGCGCTGCTGACCCCTGGAGCGC 867
QY 181 GAGCGGCGCGGGGAGAGCGCGCCACAGACCCCGGGTCCGCCGAGCAGCTGCG 240
DB 866 GAGCGGCGCGGGGAGAGCGCGCCACAGACCCCGGGTCCGCCGAGCAGCTGCG 807
QY 241 CTGTCGGGGCCAGCGCGGGCTCCAGTGGATTGCGGGGACAGACGCCAGGACCGCGCT 300
DB 806 CTGTCGGGGCCAGCGCGGGCTCCAGTGGATTGCGGGGACAGACGCCAGGACCGCGCT 747
QY 301 TCCACAGCTGGCGAGGACTGGGACCCCGGGACACCGCTCTGCCCCCTTCCAGCT 360
DB 746 TCCACAGCTGGCGAGGACTGGGACCCCGGGACACCGCTCTGCCCCCTTCCAGCT 687
QY 361 CCGCTCTCTCGCGGACCCCGCCCTCGTCCGACCCCTCCCGGTCCCGGCGCAGCC 420
DB 686 CCGCTCTCTCGCGGACCCCGCCCTCGTCCGACCCCTCCCGGTCCCGGCGCAGCC 627
QY 421 CTTCCGGGCTCTCCAGCCCTTCCCTTCTTTCGGGGCCCGCCCTCTCTCGGGCG 480
DB 626 CTTCCGGGCTCTCCAGCCCTTCCCTTCTTTCGGGGCCCGCCCTCTCTCGGGCG 567
QY 481 CGAGTTTCAGGACGCTGCTCTGTCGCGCAGTGGGAGCCCTGGCCCGGCAACCC 540
DB 566 CGAGTTTCAGGACGCTGCTCTGTCGCGCAGTGGGAGCCCTGGCCCGGCAACCC 507
QY 541 CCGGATGCGCGGCTCCCGCTGCGAGCGGCGCTCTCTGCTGCGAGCCATPAC 600
DB 506 CCGGATGCGCGGCTCCCGCTGCGAGCGGCGCTCTCTGCTGCGAGCCATPAC 447
QY 601 GCGAGTGTGCTGCGTGGCCAGCTTGTGCGGCGCTGCGGGCCCGAGGCTGGGGTGG 660
DB 446 GCGAGTGTGCTGCGTGGCCAGCTTGTGCGGCGCTGCGGGCCCGAGGCTGGGGTGG 387
QY 661 TGACGCGCGGGGACCCCGCGCTTTCGCGCGCTGCTGGGCCAGTGTGCTGTGCGTGC 720
DB 386 TGACGCGCGGGGACCCCGCGCTTTCGCGCGCTGCTGGGCCAGTGTGCTGTGCGTGC 327
QY 721 CTTGGGACGACGAGCGCCCGCCCGCTCTCTTTCGCGCAGTGGGCTCCCGGGG 780
DB 326 CTTGGGACGACGAGCGCCCGCCCGCTCTCTTTCGCGCAGTGGGCTCCCGGGG 267
QY 781 TCGGCGTCCGGCTGGGGTTGAGGGGCGCGGGGGGAACAGGCACATCGGAGGACGCG 840

DB 266 TCGGCGTCCGGCTGGGGTTGAGGGCGCGCGGGGAACAGGCACATGCGGAGAGCAGCG 207
QY 841 CAGCGGACTCAGGGCGCTTCCCGCGCAGGTGCTCTGCTGAAGAGTGTGTCGCCAGT 900
DB 206 CAGCGGACTCAGGGCGCTTCCCGCGCAGGTGCTCTGCTGAAGAGTGTGTCGCCAGT 147
QY 901 GCTGCGAGGCTCTGCGAGCGCGCGGCGGAGAGAGCTGCTGGCTTCGGCTTCGGCTGCT 960
DB 146 GCTGCGAGGCTGTGCGAGCGCGCGGCGGAGAGAGCTGCTGGCTTCGGCTTCGGCTGCT 87
QY 961 GGAAGCGGGCGCGCGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1001
DB 86 GGAAGCGGGCGCGCGGGCG 46

RESULT 2

AEA18025/c

ID AEA18025 standard; DNA; 7928 BP.

XX AEA18025;

XX AC

XX DT 11-AUG-2005 (first entry)

XX XX

XX DE Human gynecological cell proliferative disorder gene SEQ ID NO 11.

XX XX

XX KM detection; prognosis; cell proliferative disorder; cervical cancer;

XX XX endometrial cancer; neoplasia; cancer; ds.

XX OS Homo sapiens.

XX XX

XX PN WO2005049861-A2.

XX XX

XX PD 02-JUN-2005.

XX XX

XX PF 10-NOV-2004; 2004WO-EP012740.

XX XX

XX PR 10-NOV-2003; 2003EP-00025739.

XX XX

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Widschwendter M;

XX XX

XX DR WFI; 2005-396129/40.

XX XX

XX PT Detecting, differentiating, and prognosing a gynecological cell

XX PT proliferative disorder by obtaining a cervicovaginal secretion specimen

XX PT from an individual and determining the methylation status of at least one

XX PT or more CpG positions.

XX XX

XX PS Claim 3; SEQ ID NO 11; 163pp; English.

XX XX

XX CC The invention relates to a method of detecting, differentiating, and

XX CC prognosing a gynecological cell proliferative disorder comprising

XX CC obtaining a cervicovaginal secretion specimen from an individual,

XX CC determining the methylation status of at least one or more CpG positions,

XX CC and determining from the methylation status the presence, classification,

XX CC and/or prognosis of a gynecological cell proliferative disorder in the

XX CC individual. The method is useful for detecting, differentiating, and

XX CC prognosing a gynecological cell proliferative disorder, e.g. dysplasia or

XX CC low-grade squamous intraepithelial lesions, high-grade squamous

XX CC intraepithelial lesions, cervical cancer, endometrial cancer, or grade 1

XX CC to 3 cervical intraepithelial neoplasia. The present sequence represents

XX CC a human gynecological cell proliferative disorder related gene.

XX XX

SQ Sequence 7928 BP; 1629 A; 2721 C; 2411 G; 1167 T; 0 U; 0 Other;

Query Match

Best Local Similarity 100.0%; Score 1001; DB 14; Length 7928;

Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTCCGACCTGGAGGAGCCCTGGGTCTCGGATCAGGCAGCGGCAAAAGGTCCCG 60

Db 6473 C G T C G G A C C T G G A G C A G C C C T G G G T C T C G G A T C A G G C C C A A A G G G T C G C G C 6414
Qy 61 C A C G C A C C T G T T C C C A G G G C C T C C A C A T A T G G C C C C T C C C T C G G G T T A C C C C A C A G C C T 120
Db 6413 C A C G C A C C T G T T C C C A G G G C C T C C A C A T A T G G C C C C T C C C T C G G G T T A C C C C A C A G C C T 6354
Qy 121 A G G C G A T T C A C A C C T C T C C G C T G G G C C C T C G T G C G T C C C T G C A C C C T G C G A G C G C 180
Db 6353 A G G C G A T T C A C A C C T C T C C G C T G G G C C C T C G T G C G T C C C T G C A C C C T G C G A G C G C 6294
Qy 181 G A G C G G C C G C G G G G G A G C G G C C C A G A C C C C G G G T C C C C C G G A G C A G C T G C G 240
Db 6293 G A G C G G C C G C G G G G G A G C G G C C C A G A C C C C G G G T C C C C C G G A G C A G C T G C G 6234
Qy 241 C T G T C G G G C C A G G C C G G C T C C C A G T G A T T T C G G G G C A C A G A C C G C C A G A C C G C G C T 300
Db 6233 C T G T C G G G C C A G G C C G G C T C C C A G T G A T T T C G G G G C A C A G A C C G C C A G A C C G C G C T 6174
Qy 301 T C C C A C G T G G G G A G G A C T G G G A C C C G G G C A C C C G T C C T G C C C C T T C A C C T T C C A G C T 360
Db 6173 T C C C A C G T G G G A G G A C T G G G A C C C G G G C A C C C G T C C T G C C C C T T C A C C T T C C A G C T 6114
Qy 361 C G G C C T C T C G C G C G A C C C G C C C C C T C C G A C C C T C C G G G T C C C C G G C C C A G C C C 420
Db 6113 C G G C C T C T C G C G C G A C C C G C C C C C T C C G A C C C C T C C G G G T C C C C G G C C C A G C C C 6054
Qy 421 C T C C G G C C C T C C C A G C C C C T C C C T T C C T T T C G G G C C C C G C C C T C T C T C G C G G C G 480
Db 6053 C T C C G G C C C T C C C A G C C C C T C C C C T T C C T T T C G G G C C C C G C C C T C T C T C G C G G C G 5994
Qy 481 C G A G T T T C A G G C A G C G C T C G T C T G C G C A C G T G G G A A G C C C T G G C C C C C G G C A C C C 540
Db 5993 C G A G T T T C A G G C A G C G C T C G T C T G C G C A C G T G G G A A G C C C T G G C C C C G G C A C C C 5934
Qy 541 C C G G A T C G C G C G C C T C C C G C T C C C A G C C G T G C G T C C C T G T G C G A G C C A C T A C C 600
Db 5933 C C G G A T C C C G C G C T C C C G C T C C C A G C C G T G C G T C C C T G T G C G A G C C A C T A C C 5874
Qy 601 G C G A G G T C T C G C T G C G C A G T T C G T C G C G C G C C T G G G C C C C A G G C T G G C G G C T G G 660
Db 5873 G C G A G G T C T C G C T G C G C A G T T C G T G C G C G C C T G G G C C C C A G G C T G G C G G C T G G 5814
Qy 661 T G C A G C G G G G A C C C C G C G C T T T C C G C G C G C T G T G G C C C A G T G C C T G T G T G C G T G C 720
Db 5813 T G C A G C G G G G A C C C G C G C T T T C C G C G C T G T G G C C C A G T G C C T G T G T G C G T G C 5754
Qy 721 C T G G G A C G C A C G C C C C C C C C C C C C C C C T C T T C G C A G T G G G C T T C C C C G G G G 780
Db 5753 C T G G G A C G C A C G C C C C C C C C C C C C C C C T C T T C G C A G T G G G C T T C C C C G G G G 5694
Qy 781 T C G G C G T C C G C T G G G T T G A G G C G C C G G G G A A C C A G C A T G C G G A G A G C A G C G 840
Db 5693 T C G G C G T C C G C T G G G T T G A G G C G C C G G G G A A C C A G C A T G C G G A G A G C A G C G 5634
Qy 841 C A G G C A C T C A G G G C G T T C C C C C C A G G T G T C C T G C T G A A G A G C T G T G G C C C C A G T 900
Db 5633 C A G G C A C T C A G G G C G T T C C C C C C A G G T G T C C T G A A G A G C T G T G G C C C C A G T 5574
Qy 901 G C T C A G A G C T G T C G A C G C G C G C G A A A C C T G T G G C T T T C G G C T T T C G G C T G C T 960
Db 5573 G C T C A G A G C T G T C G A C G C G C G C G A A A C C T G T G G C T T T C G G C T T T C G G C T T C G C T G C T 5514
Qy 961 G A C G G G C C C G C G G G C C C C C C C G A G C C T T C A C C A C C A 1001
Db 5513 G A C G G G C C C G C G G G C C C C C C C G A G C C T T C A C C A C C A 5473

RESULT 3
AAA63785
ID AAA63785 standard; DNA; 15418 BP.
XX AC
XX AAA63785;

DT 04-DEC-2000 (first entry)
XX Nucleotide sequence of the human TERT promoter and gene from pGRN142.
XX Telomerase reverse transcriptase; TERT; promoter; telomerase complex;
XX telomere length; hyperplastic disease; cancer; oncolytic virus;
KW cis-acting transcriptional control sequence; viral replication;
KW cell proliferation; aging; immunological disorder; infertility; ss.
XX Homo sapiens.
XX WO200046355-A2.
PN 10-AUG-2000.
XX 04-FEB-2000; 2000WO-US003104.
XX 04-FEB-1999; 99US-00244438.
PR (GERO-) GERON CORP.
XX Morin GB, Lichtsteiner S, Vasserot A, Adams R, Cardoza LM;
PI Lebkowski JS;
XX WPI; 2000-532898/48.
XX New polynucleotides comprising cis-acting transcriptional control
sequences, e.g. promoter sequence, of telomerase reverse transcriptase
genes, useful in the treatment of cancer.
XX Claim 9; Page 58-61; 63pp; English.
XX The present sequence represents the human telomerase reverse
transcriptase (TERT) promoter and gene. TERT is part of the telomerase
complex responsible for maintaining telomere length and increasing
replicative capacity of progenitor cells. Telomerase activity is turned
off in mature differentiated cells, but is turned back on again in
hyperplastic diseases, including many cancers. The polynucleotide
comprises cis-acting transcriptional control sequences, e.g. promoter
sequences. These promoter sequences are used to produce oncolytic viruses,
in which a toxin or genetic element essential for viral replication is
placed under the control of a TERT promoter. As a result, the virus
replicates preferentially in cells expressing TERT, and selectively lyses
cancer cells. The oncolytic viruses are useful for treating cancer in
humans or animals. The TERT promoter sequences are useful in the
treatment of cancer and other diseases of cell proliferation such as
degenerative and aging processes and diseases of aging, immunological
disorders, or infertility
XX Sequence 15418 BP; 4518 A; 3797 C; 3765 G; 3338 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 1001; DB 3; Length 15418;
Best Local Similarity 100.0%; Pred. No. 6e-138;
Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 C G T C G G A C C T G G A G G C A G C C T G G G T C T C G G A T C A G C C A G C G G C C A A A G G G T C G C G C 60
Db 13000 C G T C G G A C C T G G A G G C A G C C T G G G T C T C G G A T C A G C C A G C C C A A A G G G T C G C G C 13059
Qy 61 C A C G C A C C T G T T C C C A G G G C C T C C A C A T C A T G G C C C C T C C C T G G G T T A C C C C A C A G C C T 120
Db 13060 C A C G C A C C T G T T C C C A G G G C C T C C A C A T C A T G G C C C C T C C C T G G G T T A C C C C A C A G C C T 13119
Qy 121 A G G C G A T T C A C A C C T C T C C G C T G G G G C C C T C G T G G C G T C C C T G C A C C C T G G G A G C G C 180
Db 13120 A G G C G A T T C A C A C C T C T C C G C T G G G G C C C T C G T G G C G T C C C T G C A C C C T G G A G C G C 13179
Qy 181 G A G C G G C C G C G G G G A A G C G C G C C C A G A C C C C G G G T C C C C C G G A G C A C T G C G 240
Db 13180 G A G C G G C C G C G G G G A A G C G C G C C C A G A C C C C C G G T C C C C C G G A G C A C T G C G 13239
Qy 241 C T G T C G G G C C A G G C C G G G C T C C C A G T G G A T T C G C G G G C A C A G A C C C C A G A C C C G C G C T 300

Db 13240 CTGTGGGGCCAGGCGGGCTCCAGTGGATTGCGGGGCACAGAGGCCACGAGCGCGCT 13299
Qy 301 TCCACAGTGGCGGAGGACTGGGGACCCGGGACACCCGCTCTGTCGCCCTTCACTTCCAGCT 360
Db 13300 TCCACAGTGGCGGAGGACTGGGGACCCGGGACACCCGCTCTGTCGCCCTTCACTTCCAGCT 13359
Qy 361 CCGGCTCTCCGCGCGAGACCCCGGCGCTCCGAGACCCCTCCGGGTCCCGGGCCGACGCC 420
Db 13360 CCGGCTCTCCGCGCGAGACCCCGGCGCTCCGAGACCCCTCCGGGTCCCGGGCCGACGCC 13419
Qy 421 CCTCCGGGCGCTCCAGCCCTCCCTTCCCTTTCGCGGGCCCGCCCTCTCTCTCGCGCG 480
Db 13420 CCTCCGGGCGCTCCAGCCCTCCCTTCCCTTTCGCGGGCCCGCCCTCTCTCTCGCGCG 13479
Qy 481 CGAGTTTCAGCGAGCGTCTGCTGCGCAGCTGGGAAGCCCTGGCCCGGCGCACCC 540
Db 13480 CGAGTTTCAGCGAGCGTCTGCTGCGCAGCTGGGAAGCCCTGGCCCGGCGCACCC 13539
Qy 541 CCGGATGCGCGGCTCCCGGCTGCGAGCGCTGCGCTCTCTGCTGGCAGCAGCTACC 600
Db 13540 CCGGATGCGCGGCTCCCGGCTGCGAGCGCTGCGCTCTCTGCTGGCAGCAGCTACC 13599
Qy 601 GCGAGGTGCTGCGGCTGCGCAGCTTCTGCGGGCCCTGGGGCCCGCAGGCTGGCGGTGG 660
Db 13600 GCGAGGTGCTGCGGCTGCGCAGCTTCTGCGGGCCCTGGGGCCCGCAGGCTGGCGGTGG 13659
Qy 661 TGCAGCGCGGGACCGCGGCTTTCGCGCGCTGCTGCGGCCAGTGTGCTGTGCGTGC 720
Db 13660 TGCAGCGCGGGACCGCGGCTTTCGCGCGCTGCTGCGGCCAGTGTGCTGTGCGTGC 13719
Qy 721 CCTGGGAGCAGCGGCGCGCGCGCGCGCGCTTTCGCGCGCTGCTGCGGCCAGTGTGCGTGC 780
Db 13720 CCTGGGAGCAGCGGCGCGCGCGCGCGCGCTTTCGCGCGCTGCTGCGGCCAGTGTGCGTGC 13779
Qy 781 TCGGCGTCCGCTGGGGTTGAGGGCGCGCGGGGAAACAGCGACATGCGGAGAGCAGCG 840
Db 13780 TCGGCGTCCGCTGGGGTTGAGGGCGCGCGGGGAAACAGCGACATGCGGAGAGCAGCG 13839
Qy 841 CAGCGACTCAGGCGCTTCCCGCGCAGGTGTCTGCTGAAGGAGCTGGTGGCGCCGAGT 900
Db 13840 CAGCGACTCAGGCGCTTCCCGCGCAGGTGTCTGCTGAAGGAGCTGGTGGCGCCGAGT 13899
Qy 901 GCTGCGAGAGCTGTGCGAGCGCGCGGCGAAGAGCTGTGCGCTTGGCTTGGCGTGTCT 960
Db 13900 GCTGCGAGAGCTGTGCGAGCGCGCGGCGAAGAGCTGTGCGCTTGGCTTGGCGTGTCT 13959
Qy 961 GCGCGGGCGCGCGGGGGCCCCCGGAGGCTTTCACCA 1001
Db 13960 GCGCGGGCGCGCGGGGGCCCCCGGAGGCTTTCACCA 14000

RESULT 4

AA138601
ID AA138601 standard; DNA; 15418 BP.
XX AC AA138601;
XX AC
XX AC
DT 16-AUG-2002 (first entry)
XX DE Human TERT promoter and upstream sequence.
XX KW Cytostatic; glycosyltransferase; tumour; cell-surface carbohydrate;
XX KW tissue specific; transcriptional control element; cancer cell;
XX KW gene therapy; human TERT; telomerase reverse transcriptase; ds.
XX OS Homo sapiens.
XX PN WO200242468-A2.
XX PD 30-MAY-2002.
XX PF 26-NOV-2001; 2001WO-US044306.
XX

PR 27-NOV-2000; 2000US-0253395P.
XX (GERO-) GERON CORP.
XX PI Schiff MJ;
XX WPI; 2002-479954/51.
XX PT New polynucleotide encoding glycosyltransferase enzymes including histo
PT blood group transferase useful for treating conditions associated with
PT hyperproliferation, such as cancers and other neoplasias.
XX PS Claim 9; Page 17-20; 49pp; English.
XX CC The invention relates to a polynucleotide comprising an encoding sequence
CC for a glycosyltransferase, under control of a heterologous tumour
CC specific or tissue specific transcriptional control element, where
CC expression of the polynucleotide in a human cell causes the cell to
CC express a cell-surface carbohydrate determinant to which some or all
CC humans have a naturally occurring antibody. The polynucleotide of the
CC invention is useful for killing cancer cells and for preparing a
CC medication for the treatment of cancer. The polynucleotide sequence of
CC the invention can be used to treat disorders by gene therapy. This
CC polynucleotide sequence represents the human TERT (telomerase reverse
CC transcriptase) promoter and upstream sequence related to the invention
XX SQ Sequence 15418 BP; 4518 A; 3797 C; 3765 G; 3338 T; 0 U; 0 Other;
Query Match 100.0%; Score 1001; DB 6; Length 15418;
Best Local Similarity 100.0%; Pred. No. 6e-138;
Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CGTCCGAGCTCGAGGAGCCCTGGGCTCCCGATCAGGCCAGCGGCAAGGCTCGCG 60
Db 13000 CGTCCGAGCTCGAGGAGCCCTGGGCTCCCGATCAGGCCAGCGGCAAGGCTCGCG 13059
Qy 61 CAGCAGCTGTTCAGAGGCTCCATCATATGAGCCCTCTCTGGGTACCCACAGCT 120
Db 13060 CAGCAGCTGTTCAGAGGCTCCATCATATGAGCCCTCTCTGGGTACCCACAGCT 13119
Qy 121 AGCGGATTCAGCTCTCTCGGTGGGGCTCGCTGGGCTCTGACCTGGAGCGC 180
Db 13120 AGCGGATTCAGCTCTCTCGGTGGGGCTCTGCTGGGCTCTGACCTGGAGCGC 13179
Qy 181 GAGCGCGCGCGGGGAGCGCGCCAGACCCCGGGTCCGCCGAGCAGCTGCG 240
Db 13180 GAGCGCGCGCGGGGAGCGCGCCAGACCCCGGGTCCGCCGAGCAGCTGCG 13239
Qy 241 CTGTGGGGCCAGCGCGGCTCCAGTGGATTGCGGGGACAGACGCCGAGCGCGCT 300
Db 13240 CTGTGGGGCCAGCGCGGCTCCAGTGGATTGCGGGGACAGACGCCGAGCGCGCT 13299
Qy 301 TCCACAGTGGCGGAGGACTGGGGACCCGGGACACCCGCTCTGCGCCCTTCACTTCCAGCT 360
Db 13300 TCCACAGTGGCGGAGGACTGGGGACCCGGGACACCCGCTCTGCGCCCTTCACTTCCAGCT 13359
Qy 361 CCGCTCTCTCCGCGCGAGACCCCGGCGCTCCGAGCCCTCCCGGGTCCCGGGCCAGCCC 420
Db 13360 CCGCTCTCTCCGCGCGAGACCCCGGCGCTCCGAGCCCTCCCGGGTCCCGGGCCAGCCC 13419
Qy 421 CTTCCGGGCGCTCCAGCCCTCTCTCTTTCGGGGCCCGCCCTCTCTCTCGCGCG 480
Db 13420 CTTCCGGGCGCTCCAGCCCTCTCTCTTTCGGGGCCCGCCCTCTCTCTCGCGCG 13479
Qy 481 CGAGTTTCAGCGAGCGTGTGCTGCTGCGCAGTGGGAAGCCCTGGCCCGGCGCACCC 540
Db 13480 CGAGTTTCAGCGAGCGTGTGCTGCTGCGCAGTGGGAAGCCCTGGCCCGGCGCACCC 13539
Qy 541 CCGGATGCGCGGCTTCCCGCTGCGAGCCGCTGCGCTCTCTGCTGCGAGCAGCTACC 600
Db 13540 CCGGATGCGCGGCTTCCCGCTGCGAGCCGCTGCGCTCTCTGCTGCGAGCAGCTACC 13599
Qy 601 GCGAGGTGCTGCGGCTGGCCAGCTTCTGCGGGCCCTGGGGGGCCCGAGGCTGGCGGTGG 660

Db 13540 CCGGATGCGCGCGCTCCCGCTGCGAGCGGTGGCTCCCTGCTGCGAGCCACTACC 13599
Qy 601 GCGAGGTGCTCCCGCTGCGCAAGTTGCTGCGCGCGCTGGGGCCCCCAGGGCTGGCGGTGG 660
Db 13600 GCGAGGTGCTCCCGCTGCGCAAGTTGCTGCGCGCGCTGGGGCCCCCAGGGCTGGCGGTGG 13659
Qy 661 TGACGCGCGGGGACCCCGCGCGCTTTTCGCGCGCTGGTGGCCAGTGTGCTGTGTGCTGTC 720
Db 13660 TGCAGCGCGGGGACCCCGCGCGCTTTTCGCGCGCTGGTGGCCAGTGTGCTGTGTGCTGTC 13719
Qy 721 CCTGGGACGACAGCG 780
Db 13720 CCTGGGACGACAGCG 13779
Qy 781 TCGCGCTCCCGCTGGGTGTAGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 840
Db 13780 TCGCGCTCCCGCTGGGTGTAGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 13839
Qy 841 CAGCGCACTCAGGCGCGCTTCCCGCGAGGTGCTCTGCTGAAGAGCTGTGGCGCGCGT 900
Db 13840 CAGCGCACTCAGGCGCGCTTCCCGCGAGGTGCTCTGCTGAAGAGCTGTGGCGCGCGT 13899
Qy 901 GCTGACAGGCTGTGCGAGCG 960
Db 13900 GCTGACAGGCTGTGCGAGCG 13959
Qy 961 GGACGGGCG 1001
Db 13960 GGACGGGCG 14000

RESULT 6

AAL38595
ID AAL38595 standard; DNA; 15418 BP.
XX
AC AAL38595;
XX
DT 16-AUG-2002 (first entry)
XX
DE DNA of plasmid pGRN144 containing human hTERT gene.
XX
KW Anticonvulsant; cerebroprotective; vasotropic; nootropic; stem cell;
KW neuroprotective; antiparkinsonian; antiinflammatory; undifferentiated;
KW cardiant; transcriptional control element; human embryonic; tissue graft;
KW regenerative medicine; tissue reconstitution; neural progenitor cell;
KW nerve system; epilepsy; stroke; ischaemia; Huntington's disease;
KW Parkinson's disease; multiple sclerosis; leukodystrophy; neuritis;
KW hepatocyte; liver damage; cardiomyocyte; cryoinjury; cardiac muscle;
KW pGRN144; human hTERT gene; chimeric; ds.
XX
OS Homo sapiens.
OS Unidentified.
OS Chimeric.
XX
PN W0200242445-A2.
XX
PD 30-MAY-2002.
XX
XX 26-NOV-2001; 2001WO-US044309.
XX
XX 27-NOV-2000; 2000US-0253357P.
PR 27-NOV-2000; 2000US-0253443P.
PR 13-FEB-2001; 2001US-00783203.
XX
XX (GERO-) GERON CORP.
XX
XX Gold JD, Lebrowski JS;
XX WPI; 2002-479952/51.
DR
XX Depleting a cell e.g., human embryonic stem cell population of
PT undifferentiated stem cells (UC) for use in regenerative medicine
PT comprises genetically altering UC in a population to express nucleic acid

encoding a lethal product.
Example 9; Page 62-66; 67pp; English.
The invention relates to a system for depleting a cell population of undifferentiated stem cells, by introducing nucleic acids of structure P-X, where X is a nucleic acid encoding product that is lethal to a cell in which it is expressed; or renders a cell in which it is expressed susceptible to the lethal effect of an external agent, and P is a transcriptional control element causing X to be preferentially expressed in the undifferentiated stem cells. The system is used for depleting a cell population (preferably, human embryonic stem cells) of undifferentiated stem cells. A population of differentiated cells is useful in regenerative medicine, and for preparing antibodies and cDNA libraries that are specific for a differentiated phenotype. The cell populations are also useful for drug screening and therapeutic applications. The differentiated cells are useful for tissue reconstitution or regeneration in a human patient in need of treatment. The cells are administered in a manner that permits to graft to the intended tissue side and reconstitute or regenerate the functionally deficient area. The neural progenitor cells are useful for treating acute or chronic damage to the nerve system e.g. epilepsy, stroke, ischaemia, Huntington's disease, Parkinson's disease, multiple sclerosis, leukodystrophies, neuritis, etc. The hepatocytes and hepatocyte precursors are useful for assessing animal models for ability to repair liver damage. The cardiomyocyte population is useful for assessing animal models for cryoinjury, regenerating cardiac muscle and to treat insufficient cardiac function. This polynucleotide sequence represents the DNA of plasmid pGRN144 containing the human hTERT gene relating to the invention
XX
SQ Sequence 15418 BP; 4519 A; 3797 C; 3764 G; 3338 T; 0 U; 0 Other;
Query Match 100.0%; Score 1001; DB 6; Length 15418;
Best Local Similarity 100.0%; Pred. No. 6e-138;
Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CGTCCGACCTGGAGGAGCCCTGGGTCTCGGATCAGGCGAGGCGCAAGGTGCGCG 60
Db 13000 CGTCCGACCTGGAGGAGCCCTGGGTCTCGGATCAGGCGAGGCGCAAGGTGCGCG 13059
Qy 61 CAGCACCTGTTCCAGGGGCTCCACATATGCCCCCTCCCTGGGGTTACCCACAGCCT 120
Db 13060 CAGCACCTGTTCCAGGGGCTCCACATATGCCCCCTCCCTGGGGTTACCCACAGCCT 13119
Qy 121 AGGCCGATTGACCTCTCTCCGTGGGGCCCTCGCTGGCGTCCCTGCACCTGGGAGCGC 180
Db 13120 AGGCCGATTGACCTCTCTCCGTGGGGCCCTCGCTGGCGTCCCTGCACCTGGGAGCGC 13179
Qy 181 GAGCGGCGCGGGGGAAGCGCGGCCACAGACCCCGGGTCCGCCGAGCAGCTGCG 240
Db 13180 GAGCGGCGCGGGGGAAGCGCGGCCACAGACCCCGGGTCCGCCGAGCAGCTGCG 13239
Qy 241 CTGTGCGGGCCAGCGCGGGTCCAGTGGATTGCGGGCACACAGCCCGAGGACCGCGCT 300
Db 13240 CTGTGCGGGCCAGCGCGGGTCCAGTGGATTGCGGGCACACAGCCCGAGGACCGCGCT 13299
Qy 301 TCCACGTTGCGGAGGAGCTGGGGACCCGGGCAACCCGCTCTCTGCCCCCTTCACCTTCAGCT 360
Db 13300 TCCACGTTGCGGAGGAGCTGGGGACCCGGGCAACCCGCTCTCTGCCCCCTTCACCTTCAGCT 13359
Qy 361 CCGCTCTCTCGGCGGAGACCCCGCGCGCTCCAGACCCCTCCCGGGTCCCGGCCCAGGCC 420
Db 13360 CCGCTCTCTCGGCGGAGACCCCGCGCGCTCCAGACCCCTCCCGGGTCCCGGCCCAGGCC 13419
Qy 421 CTTCCGGGGCCCTCCAGCCCTCCCTTTCTTTCGGGGCCCGCCCTCTCTCTCGCGCG 480
Db 13420 CTTCCGGGGCCCTCCAGCCCTCCCTTTCTTTCGGGGCCCGCCCTCTCTCTCGCGCG 13479
Qy 481 CGAGTTTCAGGCGCGCTGCGTCTGTGCGCAAGGAGCCCTGGCCCGGCCACCC 540
Db 13480 CGAGTTTCAGGCGCGCTGCGTCTGTGCGCAAGGAGCCCTGGCCCGGCCACCC 13539


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Qy 601 GCGAGGTGCTGCGCTGCGTCACAGTTCGTGCGGCGCTTGGGGCCCCCAGGCTGGCGGCTGG 660
Db |||||||
13600 GCGAGGTGCTGCGCTGCGTCACAGTTCGTGCGGCGCTTGGGGCCCCCAGGCTGGCGGCTGG 13659
Qy 661 TGCAGCGCGGGAGACCGCGCGCTTTCGCGCGCTGTGTGGCGCCAGTGCCTGTGTGCTGTC 720
Db |||||||
13660 TGCAGCGCGGGAGACCGCGCGCTTTCGCGCGCTGTGTGGCGCCAGTGCCTGTGTGCTGTC 13719
Qy 721 CCTGGGAGCGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 780
Db |||||||
13720 CCTGGGAGCGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 13779
Qy 781 TCGCGCTGCTGCGCTGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 840
Db |||||||
13780 TCGCGCTGCTGCGCTGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 13839
Qy 841 CAGCGGACTCAGGCGCGCTTCCCGCGCGAGTGTCTGCTGCTGAAGAGCTGTGTGCGCGCG 900
Db |||||||
13840 CAGCGGACTCAGGCGCGCTTCCCGCGCGAGTGTCTGCTGCTGAAGAGCTGTGTGCGCGCG 13899
Qy 901 GCTGCAGAGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 960
Db |||||||
13900 GCTGCAGAGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 13959
Qy 961 GGACGGGGCGCGCGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1001
Db |||||||
13960 GGACGGGGCGCGCGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 14000
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RESULT 8

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ADU82631
ID ADU82631 standard; DNA; 5491 BP.
AC ADU82631;
XX
XX 10-FEB-2005 (first entry)
XX Human hTERT gene nucleotide sequence.
XX
XX Gene expression; transcription; TERT; telomerase reverse transcriptase;
XX cancer therapy; cytoskeletal; CNS; respiratory; anti-HIV; antianemic;
XX antisickling; hemostatic; antidiabetic; cardiant; antiinflammatory;
XX antirheumatic; antiarthritic; neuroprotective; antiasthmatic; vasotropic;
XX gene therapy; apoptosis stimulator; cancer; gene; ds.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 3415..3633
XX /*tag= a
XX /product= "telomerase reverse transcriptase fragment"
XX /partial
XX
XX W02004099377-A2.
XX
XX 18-NOV-2004.
XX
XX 30-APR-2004; 2004WO-US013487.
XX
XX 01-MAY-2003; 2003US-0467171P.
XX (MUSC-) MUSC FOUND RES DEV.
XX
XX Dong J, Rubinchik S, Woraratanadham J;
XX
XX WPI; 2004-805118/79.
XX P-PSDB; ADU82632.
XX GENBANK; AB016767.
XX
XX New expression vector comprising a first expression cassette with a first
XX coding region that encodes a transcriptional activating factor (TAP),
XX useful in treating cancer, AIDS, hemophilia, diabetes and asthma.
```

```
PS
XX
CC
CC The invention relates to an expression vector comprising a first
CC expression cassette having a first coding region that encodes a
CC transcriptional activating factor (TAP), and a second expression cassette
CC comprising a second coding region that encodes a selected polypeptide.
CC The expression vector further comprises a first expression cassette
CC having a first coding region that encodes a transcriptional activating
CC factor (TAP), the first coding region being positioned under the
CC transcriptional control of a first promoter comprising a tissue specific
CC regulatory element (TSRE), and a TAP binding site (TBS), and a second
CC expression cassette comprising a second coding region that encodes a
CC selected polypeptide, the second coding region being positioned under the
CC transcriptional control of a second promoter comprising a TSRE and a TBS,
CC or a TBS. The expression vector further comprises a third coding region
CC that encodes a first transcriptional silencer (TSI), the third coding
CC region being positioned under the transcriptional control, a third
CC promoter comprising a TSRE and a TAB, and a fourth expression cassette
CC comprising a fourth coding region that encodes a second TSI, the fourth
CC coding region being positioned under the transcriptional control of a
CC fourth promoter that is negatively regulated by the first TSI, where the
CC first, second and third promoters are negatively regulated by the second
CC TSI. The selected polypeptide is a therapeutic polypeptide, such as an
CC anti-cancer polypeptide that is a tumor suppressor, and inducer of
CC apoptosis, and cell cycle regulator, a toxin, or an inhibitor of
CC angiogenesis, and an enzyme, a cytokine, a hormone, a tumor antigen, a
CC human antigen or a pathogen antigen. The selected polypeptide is
CC essential for vector replication, where the vector is an adenoviral
CC vector. The expression vector is useful in methods for treating cancer
CC and further comprises a selectable or screenable marker. The methods and
CC compositions of the present invention are useful in the fields of
CC molecular biology and gene therapy, particularly to the combined spatial
CC and quantitative regulation of transgene expression in eukaryotic cells,
CC and in treating cancer including breast cancer, ovarian cancer, fallopian
CC cancer, pancreatic cancer, colon cancer, bladder cancer, liver cancer,
CC stomach cancer, lung cancer, lymphoid cancer, brain cancer, thyroid
CC cancer, head and neck cancer, skin cancer or leukemia. The cancer is a
CC recurrent cancer, a metastatic cancer or a drug resistant cancer. The
CC methods and compositions can also be used in treating cystic fibrosis,
CC AIDS, sickle cell anemia, rheumatoid arthritis, multiple sclerosis, asthma
CC inflammatory disorders, hemophilia, diabetes, heart disease,
CC and restenosis. The present sequence represents a human telomerase
CC reverse transcriptase (hTERT) gene nucleotide sequence, the promoter
CC fragment can be used in the vectors of the invention.
XX
XX SQ Sequence 5491 BP; 954 A; 1729 C; 1677 G; 1131 T; 0 U; 0 Other;
```

```
Query Match 99.8%; Score 999.4; DB 13; Length 5491;
Best Local Similarity 99.9%; Pred. No. 1.2e-137;
Matches 1000; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGTCCGACCTGGAGGAGCGCCCTGGGTCTCCGATCAGGCCAGCGGCAAGGCTCGCCG 60
Db |||||||
2870 CGTCCGACCTGGAGGAGCGCCCTGGGTCTCCGATCAGGCCAGCGGCAAGGCTCGCCG 2929

Qy 61 CAGCGACCTGTTCAGGAGCGCTCCATCATGTGCGCCCTCCCTCGGGTACCCACAGCCT 120
Db |||||||
2930 CAGCGACCTGTTCAGGAGCGCTCCATCATGTGCGCCCTCCCTCGGGTACCCACAGCCT 2989

Qy 121 AGGCCGATTGAGCTCTCTCCGCTGGGGCGCTCGCTGGCGCTCCCTGACCCCTGGGAGCGC 180
Db |||||||
2990 AGGCCGATTGAGCTCTCTCCGCTGGGGCGCTCGCTGGCGCTCCCTGACCCCTGGGAGCGC 3049

Qy 181 GAGCGCGCGCGCGCGGGGAAAGCGCGGCCAGACCCCGGGTCCGCCGAGCAGCTGCG 240
Db |||||||
3050 GAGCGCGCGCGCGCGGGGAAAGCGCGGCCAGACCCCGGGTCCGCCGAGCAGCTGCG 3109

Qy 241 CTGTCCGGGGCAGCGCGGCTCCAGTGGATTGCGGGGACAGCGCCCGGCGCTCG 300
Db |||||||
3110 CTGTCCGGGGCAGCGCGGCTCCAGTGGATTGCGGGGACAGCGCCCGGCGCTCG 3169

Qy 301 TCCACGTGGCGGAGGAGCTGGGGACCCGGGGACCCGCTCCTGCGCCCTTCCACCTCCAGCT 360
```

Db	3170	CCCCACGTGGCGGAGGACTGGGACCCGCGACACCGTCTCTGCCCCCTTCACCTTCCAGCT	3229	FT	exon	/*tag= c /number= 1
Qy	361	CCGCTCTCTCCGCGGAGACCCGCGGCTCCGAGACCTCCCGGGTCCCGGCCACGCC	420	FT	FT	/*tag= d /number= 2
Db	3230	CCGCTCTCTCCGCGGAGACCCGCGGCTCCGAGACCTCCCGGGTCCCGGCCACGCC	3289	FT	intron	/*tag= e /number= 2
Qy	421	CCTCGGCGCCCTCCAGCCCTCCCTTCCCTTTCCGCGGCGCCCGCCCTCTCTCGCGCG	480	FT	exon	/*tag= f /number= 3
Db	3290	CCTCGGCGCCCTCCAGCCCTCCCTTCCCTTTCCGCGGCGCCCGCCCTCTCTCGCGCG	3349	FT	FT	/*tag= g /number= 3
Qy	481	CGAGTTTCAGGACGCTGCTCTGCTGCGACAGTGGGAGGCCCTGGCCCGGCCACCC	540	FT	intron	/*tag= h /number= 4
Db	3350	CGAGTTTCAGGACGCTGCTCTGCTGCGACAGTGGGAGGCCCTGGCCCGGCCACCC	3409	FT	exon	/*tag= i /number= 4
Qy	541	CCGCGATGCCGCGCTCCCGCTGCGAGCGTGGCTCCCTGCTGCGGACGACCTACC	600	FT	intron	/*tag= j /number= 5
Db	3410	CCGCGATGCCGCGCTCCCGCTGCGAGCGTGGCTCCCTGCTGCGGACGACCTACC	3469	FT	FT	/*tag= k /number= 5
Qy	601	GCAGGCTGCTCCGCTGGCCACAGTTCCGTGCGCGCGCTGGGCGCCAGGGCTGGCGGCTGG	660	FT	exon	/*tag= l /number= 6
Db	3470	GCAGGCTGCTCCGCTGGCCACAGTTCCGTGCGCGCGCTGGGCGCCAGGGCTGGCGGCTGG	3529	FT	intron	/*tag= m /number= 6
Qy	661	TGCAGCGCGGAGACCCCGCGGCTTTCCGCGGCTGGTGGCCAGTGCCTGTGTGCTGTC	720	FT	exon	/*tag= n /number= 7
Db	3530	TGCAGCGCGGAGACCCCGCGGCTTTCCGCGGCTGGTGGCCAGTGCCTGTGTGCTGTC	3589	FT	FT	/*tag= o /number= 7
Qy	721	CCTGGGAGGACGCGCGCGCCCGCGCGCTCCCTTCCGCGAGTGGGCTCCCGCGGG	780	FT	intron	/*tag= p /number= 8
Db	3590	CCTGGGAGGACGCGCGCGCCCGCGCGCTCCCTTCCGCGAGTGGGCTCCCGCGGG	3649	FT	exon	/*tag= q /number= 8
Qy	781	TCGCGCTCCGCTGGGGTTGAGGGCGGCGCGGGGGAACAGCGACATGCGGAGAGAGCG	840	FT	intron	/*tag= r /number= 9
Db	3650	TCGCGCTCCGCTGGGGTTGAGGGCGGCGCGGGGGAACAGCGACATGCGGAGAGAGCG	3709	FT	FT	/*tag= s /number= 9
Qy	841	CAGCGGACTCAGGCGCTTCCCGCGAGGTTCCTGCTGAAGGAGCTGGTGGCCCGAGT	900	FT	exon	/*tag= t /number= 10
Db	3710	CAGCGGACTCAGGCGCTTCCCGCGAGGTTCCTGCTGAAGGAGCTGGTGGCCCGAGT	3769	FT	intron	/*tag= u /number= 10
Qy	901	GCTCAGAGGCTGTGAGCGCGCGCGGAGAAAGTGTGCTGGCTTCGGCTTCGCGCTGCT	960	FT	exon	/*tag= v /number= 11
Db	3770	GCTCAGAGGCTGTGAGCGCGCGCGGAGAAAGTGTGCTGGCTTCGCGCTTCGCGCTGCT	3829	FT	intron	/*tag= w /number= 11
Qy	961	GGACGGGCGCGCGGCGCGCGCGCGCGCGCGCTTCCACCA	1001	FT	exon	/*tag= x /number= 12
Db	3830	GGACGGGCGCGCGGCGCGCGCGCGCGCGCGCTTCCACCA	3870	FT	FT	/*tag= y /number= 12
RESULT 9						
ID	AAS96607 standard; DNA; 51552 BP.					
XX	AAS96607;					
AC	AAS96607;					
XX	09-APR-2002. (first entry)					
DT	DNA encoding human telomerase reverse transcriptase (TERT) #1.					
DE	Telomerase reverse transcriptase; TERT; cytosolic; apoptosis;					
XX	cell growth inhibitor; antisense oligonucleotide; antisense technology;					
KW	ds.					
XX	Homo sapiens.					
OS	Key					
XX	Location/Qualifiers					
FT	1. .11492					
FT	/*tag= a					
FT	/number= 1					
FT	11274. .47813					
FT	/*tag= b					
FT	/product= "TERT"					
FT	/note= "Telomerase reverse transcriptase"					
FT	11493. .11596					
FT	intron					

FT exon /number= 13
46130. .46254
/*tag= ab
FT intron /number= 14
46255. .47035
/*tag= ac
FT exon /number= 14
47036. .47173
/*tag= ad
FT intron /number= 15
47174. .47709
/*tag= ae
FT intron /number= 15
47710. .50544
/*tag= af
FT /number= 16

WO200188198-A1.

22-NOV-2001.

15-MAY-2001; 2001WO-US015774.

16-MAY-2000; 2000US-00572423.

07-DEC-2000; 2000US-00733294.

(ISIS-) ISIS PHARM INC.

Monia BP, Gaarde WA, Freier SM, Wanciewicz E;

WPI; 2002-075321/10.

P-PSDB; AAU72735.

New compound targeted to nucleic acid molecule encoding telomerase transcriptase (TERT), which specifically hybridizes with and inhibits expression of TERT, useful for modulating apoptosis and inhibiting cell growth.

Example 19; Page 112-138; 154pp; English.

The invention describes a compound, 8-50 nucleobases in length targeted to a nucleic acid molecule encoding human TERT (telomerase reverse transcriptase), where the compound specifically hybridizes with and inhibits the expression of TERT. A series of oligonucleotides were designed to target different regions of the human TERT RNA. These were 20 nucleotides in length and composed of a central gap region consisting of ten 2'-deoxynucleotides, flanked on both sides (5' and 3' directions) by five-nucleotide wings. The wings were composed of 2'-methoxyethyl (2'-MOE) nucleotides. The compounds were analysed for their effect on human TERT mRNA levels by reverse transcriptase (RT)-polymerase chain reaction (PCR). The compound is useful for inhibiting the expression of TERT in cells or tissues, for treating a human having disease or condition associated with TERT, for modulating apoptosis, for inhibiting cell growth (preferably, cancer cell growth), in antisense therapy and for diagnostics and therapeutics. This sequence encodes human telomerase reverse transcriptase (TERT) #1, and is used to create antisense oligonucleotides which modify TERT expression, described in the method of the invention

Sequence 51552 BP; 10709 A; 13313 C; 15370 G; 12158 T; 0 U; 2 Other;

Query Match 99.8%; Score 999.4; DB 6; Length 51552;
Best Local Similarity 99.9%; Pred. No. 8.4e-138;
Matches 1000; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 CGTCCGACCTGGAGGCGAGCCCTGGGGTCTCCGGATCAGGCGCAGCGCCAAAGGGTCCCG 60
Db 10729 CGTCCGACCTGGAGGCGAGCCCTGGGGTCTCCGGATCAGGCGCAGCGCCAAAGGGTCCCG 10788
Qy 61 CAGCACCTGTTCCAGGGGCTCCACATCATATGGCCCTCCCTGGGGTTACCCACAGCCT 120
Db 10789 CAGCACCTGTTCCAGGGGCTCCACATCATATGGCCCTCCCTGGGGTTACCCACAGCCT 10848

Qy 121 AGGCCGATTTCGACCTCTCTCCGCTGGGGCCCTCGCTGGGGCTCCCTGCACCTTGGAGCGC 180
Db |||||
10849 AGGCCGATTTCGACCTCTCTCCGCTGGGGCCCTCGCTGGGGCTCCCTGCACCTTGGAGCGC 10908
Qy 181 GAGCGCGCGCGCGCGGGAAGCGCGGCCAGACCCCGGGTCCGCCCGAGCAGCTGCG 240
Db |||||
10909 GAGCGCGCGCGCGCGGGAAGCGCGGCCAGACCCCGGGTCCGCCCGAGCAGCTGCG 10968
Qy 241 CTGTCCGGGCGCAGCGCGGGCTCCACGTGGATTTCGGGGGCAACAGCCCGAGGACCGCGCT 300
Db |||||
10969 CTGTCCGGGCGCAGCGCGGGCTCCACGTGGATTTCGGGGGCAACAGCCCGAGGACCGCGCT 11028
Qy 301 TCCACAGTGGCGGAGGACCTGGGGACCCCGGGACCCGCTCTGCTGCCCTTCACTTCCAGCT 360
Db |||||
11029 CCCACAGTGGCGGAGGACCTGGGGACCCCGGGACCCGCTCTGCTGCCCTTCACTTCCAGCT 11088
Qy 361 CGGCTCTCTCCGCGCGGACCCCGCCCGCTCCGACCCCTCCCGGGTCCCGGGCCAGCCCC 420
Db |||||
11089 CGGCTCTCTCCGCGCGGACCCCGCCCGCTCCGACCCCTCCCGGGTCCCGGGCCAGCCCC 11148
Qy 421 CTTCCGGGCGCTCCAGACCCCTCCCTTCTTTCGGGGCCCGCGCTCTCTTGGGGCG 480
Db |||||
11149 CTTCCGGGCGCTCCAGACCCCTCCCTTCTTTCGGGGCCCGCGCTCTCTTGGGGCG 11208
Qy 481 CGAGTTTTCAGGCGAGCTGCTGCTGCTGCGCACGCTGGGGAAGCCCTGGGCCCGGCCACCC 540
Db |||||
11209 CGAGTTTTCAGGCGAGCTGCTGCTGCTGCGCACGCTGGGGAAGCCCTGGGCCCGGCCACCC 11268
Qy 541 CGCGATGCGCGCGCTCCCGCTGCGAGCCGCTGCGCTCCCTGCTGCGGAGCAGCTTACC 600
Db |||||
11269 CGCGATGCGCGCGCTCCCGCTGCGAGCCGCTGCGCTCCCTGCTGCGGAGCAGCTTACC 11328
Qy 601 GCGAGTGTCTGCGCGTGGCCACGTTGCTGGGGCGCTGGGGCCCGAGGGCTGGGGCTGG 660
Db |||||
11329 GCGAGTGTCTGCGCGTGGCCACGTTGCTGGGGCGCTGGGGCCCGAGGGCTGGGGCTGG 11388
Qy 661 TGCAGCGCGGGGACCCCGGGGGCTTTCCGGCGCTGCTGGGCCAGTGTGCTGCTGCTGCTGC 720
Db |||||
11389 TGCAGCGCGGGGACCCCGGGGGCTTTCCGGCGCTGCTGGGCCAGTGTGCTGCTGCTGCTGC 11448
Qy 721 CTTGGGACGACGCGCGCGCCCGCGCGCTTCTTCCGCCAGGTGGGCTTCCCGGGG 780
Db |||||
11449 CTTGGGACGACGCGCGCGCCCGCGCGCTTCTTCCGCCAGGTGGGCTTCCCGGGG 11508
Qy 781 TCGGCTTCCGCTGGGGTTCAGGGCGCGCGGGGGGAAACGACGACATCGCGAGAGCAGCG 840
Db |||||
11509 TCGGCTTCCGCTGGGGTTCAGGGCGCGCGGGGGGAAACGACGACATCGCGAGAGCAGCG 11568
Qy 841 CAGGCGACTCAGGGCGCTTCCCGCGCAGGTGTCTGCTGAAGGAGCTGCTGGGCCCGAGT 900
Db |||||
11569 CAGGCGACTCAGGGCGCTTCCCGCGCAGGTGTCTGCTGAAGGAGCTGCTGGGCCCGAGT 11628
Qy 901 GCTGCAGAGCTGTGCGAGCGCGCGGAGAAACGCTGCTGGCTTCCGGCTTCCGGCTTCCGCT 960
Db |||||
11629 GCTGCAGAGCTGTGCGAGCGCGCGGCGGAAACGCTGCTGGCTTCCGGCTTCCGGCTTCCG 11688
Qy 961 GGAAGGGGGCGCGGG 1001
Db |||||
11689 GGAAGGGGGCGCGGG 11729

RESULT 10

AAV16979

ID AAV16979 standard; DNA; 4335 BP.

XX AAV16979;

DT 13-AUG-1998 (first entry)

XX Human telomerase reverse transcriptase genomic clone.

DE Human telomerase reverse transcriptase; hTERT; TERT; diagnosis; prognosis;

KW Human; telomerase reverse transcriptase; hTERT; TERT; diagnosis; prognosis;

KW cell proliferation; cancer; ageing; ribonucleoprotein; ss.

XX Homo sapiens.
OS GB2317891-A.
PN
XX
XX 08-APR-1998.
XX
XX 01-OCT-1997; 97GB-00020890.
XX
XX 01-OCT-1996; 96US-00724643.
PR 18-APR-1997; 97US-00844419.
PR 25-APR-1997; 97US-00846017.
PR 06-MAY-1997; 97US-00851843.
PR 09-MAY-1997; 97US-00854050.
PR 14-AUG-1997; 97US-00911312.
PR 14-AUG-1997; 97US-00912951.
PR 14-AUG-1997; 97US-00915503.
XX
XX (GERO-) GERON CORP.
PA (UYTE-) UNIV TECHNOLOGY CORP.
PA
XX
XX Cech TR, Lingner J, Nakamura T, Chapman KB, Morin GB, Harley CB;
PI Andrews WH;
XX
XX WPI; 1998-171633/16.
DR
XX
XX Pure and recombinant human Telomerase Reverse Transcriptase and its
PT variants - are useful in the diagnosis, prognosis and treatment of cell
PT proliferation conditions especially cancer and ageing.
XX
XX Example 3; Fig 21; 387pp; English.
PS
XX
XX The present sequence represents a human telomerase reverse transcriptase
CC (hTERT) genomic clone from the present invention. The present invention
CC also describes the following methods: (A) determining whether a test
CC compound is a modulator of hTERT, by detecting the change in hTERT
CC recombinant protein or polynucleotide, on administration of the compound;
CC (B) preparation of recombinant telomerase by contacting a protein
CC preparation of hTERT with a telomerase RNA component; (C) detection of the
CC hTERT RNA or protein in a sample by binding a relevant probe to the sample
CC and detecting the complex formed or in the case of RNA detection,
CC amplifying the product and correlating the presence of complex or
CC amplification product with presence of hTERT in the sample; and (D)
CC increasing the proliferation of a vertebrate cell by increasing hTERT
CC expression; and (E) the use of an agent that causes an increase in cell
CC vertebrate cell proliferation to create a medicament that inhibits
CC ageing. A protein preparation of hTERT and the polynucleotide encoding
CC hTERT can be used in the manufacture of medicaments for inhibiting the
CC effect of ageing or cancer. Inhibitors of telomerase activity can be used
CC to treat conditions that are associated with high telomerase activity. A
CC protein preparation of hTERT can also be used in the new methods
XX
XX Sequence 4335 BP; 698 A; 1416 C; 1360 G; 861 T; 0 U; 0 Other;
SQ
Query Match 94.5%; Score 945.8; DB 2; Length 4335;
Best Local Similarity 98.9%; Pred. No. 8.5e-130;
Matches 994; Conservative 0; Mismatches 7; Indels 4; Gaps 4;
QY 1 COTCCGGACCTGGAGGCGAGCCCTCGGCTCTCCGGATCAGGCCAGCGGCCAAGAGGTCGCGC 60
Db 1947 CGTCCGGACCTGGAGGCGAGCCCTCGGCTCTCCGGATCAGGCCAGCGGCCAAGAGGTCGCGC 2006
QY 61 CAGCGACCTGTTCCAGGCGCTTCCATCATCATGCGCCCTCCCTCGGGTTACCCACAGGCT 120
Db 2007 CAGCGACCTGTTCCAGGCGCTTCCATCATCATGCGCCCTCCCTCGGGTTACCCACAGGCT 2066
QY 121 AGGCCGATTGCACTCTCTCCGCTGGGGCCCTCGCTGGGCTCCCTGCACTCCCTGGAGGCGC 180
Db 2067 AGGCCGATTGCACTCTCTCCGCTGGGGCCCTCGCTGGGCTCCCTGCACTCCCTGGAGGCGC 2126
QY 181 GAGCGCGCGCGGGGGGGAAGCGGGGCCAGACCCCGCGGTCGCGCCGCGAGCAGCTGG 240
Db 2127 GAGCGCGCGCGGGGGGGAAGCGGGGCCAGACCCCGCGGTCGCGCCGCGAGCAGCTGG 2186

QY	241	CTGTGGGGCCAGGCGCGGGCTCCAGTGAGATTGGCGGC-ACAGAGCCAGGACCGGCG	299
Db	2187	CTGTGGGGCCAGGCGCGGGCTCCAGTGAGATTGGCGGCACAGAGCCAGGACCGGCG	2246
QY	300	TTCCACGTGGCGGAGGAGTGGGACCCGGGACCGGTCTCTGCTCCCTTACCTTCAGC	359
Db	2247	TTCCACGTGGCGGAGGAGTGGGACCCGGGACCGGTCTCTGCTCCCTTACCTTCAGC	2306
QY	360	TGCGCTCTCCCGCGCG-ACCCCGCGCGTCCCG-ACCCCTCCCGGTCCCGCGCCAG	417
Db	2307	TCCGCTCTGGTCCGCGCGAACC CGCCCGTCCCGAACCTTCCCGGGTCCCGCGCCAG	2365
QY	418	CCCCCTCCGGGCGCTCCAGCCCTCCCTTCC-TTTCGGCGGCGCCGCTCTCTCTCGC	476
Db	2367	CCCCCTCCGGGCGCTCCAGCCCTCCCTTCC-TTTCGGCGGCGCCGCTCTCTCTCGC	2426
QY	477	GGCGGAGTTTCAGGACGCGTCTGCTGTCGCGACGTGGGAAGCCCTGGCGCCGCGC	536
Db	2427	GGCGGAGTTTCAGGACGCGTCTGCTGTCGCGACGTGGGAAGCCCTGGCGCCGCGC	2486
QY	537	ACCCCGCGGATGCGCGCGCTCCCGCTGCGAGCGCTCCCTCTGCTGCGAGCCAC	596
Db	2487	ACCCCGCGGATGCGCGCGCTCCCGCTGCGAGCGCTCCCTCTGCTGCGAGCCAC	2546
QY	597	TACCGCGAGGTGCTGCGCTGGCCACGTTCTGTGGCGGCTTGGGCGCCAGGGCTGGCGG	656
Db	2547	TACCGCGAGGTGCTGCGCTGGCCACGTTCTGTGGCGGCTTGGGCGCCAGGGCTGGCGG	2606
QY	657	CTGTGACGCGCGGAGACCGCGGCTTTCGCGGCTGTGGTGGCCAGTCCCTGTGTGC	716
Db	2607	CTGTGACGCGCGGAGACCGCGGCTTTCGCGGCTGTGGTGGCCAGTCCCTGTGTGC	2666
QY	717	GTGCGCTGGAGACGCGCGCGCCCGCGCGCTCCCTCTGCGCGAGTGGGCTCCCG	776
Db	2667	GTGCGCTGGAGACGCGCGCGCCCGCGCGCTCCCTCTGCGCGAGTGGGCTCCCG	2726
QY	777	GGGCTCGCGCTGCGGCTGGGTTGAGGCGCGCGCGGGAACAGCGACATGCGGAGAGC	836
Db	2727	GGGCTCGCGCTGCGGCTGGGTTGAGGCGCGCGCGGGAACAGCGACATGCGGAGAGC	2786
QY	837	AGCGGAGCGGACTCAGGCGGCTTCCCGCGAGGTGCTCTGCTGAAGAGCTGTGTGGCC	896
Db	2787	AGCGGAGCGGACTCAGGCGGCTTCCCGCGAGGTGCTCTGCTGAAGAGCTGTGTGGCC	2846
QY	897	GAGTCTGCAGAGCTGTCCAGCGCGCGCGGAGAGTGTGCTTGGCTTCCGCTTCGCGC	956
Db	2847	GAGTCTGCAGAGCTGTCCAGCGCGCGCGGAGAGTGTGCTTGGCTTCCGCTTCGCGC	2906
QY	957	TGCTGGAGCGGGCGCGCGGGCGCCCGCGAGGCTTCCACCA 1001	
Db	2907	TGCTGGAGCGGGCGCGCGGGCGCCCGCGAGGCTTCCACCA 2951	
RESULT 11			
ADU82633			
ID	ADU82633	standard; DNA; 4356 BP.	
XX	AC	ADU82633;	
XX	DT	10-FEB-2005 (first entry)	
XX	DE	Human hTERT gene nucleotide sequence.	
XX	KW	Gene expression; transcription; TERT; telomerase reverse transcriptase;	
XX	KW	cancer therapy; cytostatic; CNS; respiratory; anti-HIV; antianemic;	
XX	KW	antisickling; hemostatic; antidiabetic; cardiac; antiinflammatory;	
XX	KW	antirheumatic; antiarthritic; neuroprotective; antiasthmatic; vasotropic;	
XX	OS	gene therapy; apoptosis stimulator; cancer; gene; da.	
XX	OS	Homo sapiens.	
XX	XX	Key	Location/Qualifiers
XX	XX	Key	Location/Qualifiers

FT CDS 3997. .4215
FT /*tag= a
FT /product= "telomerase reverse transcriptase fragment"
FT /partial
XX W02004099377-A2.
XX 18-NOV-2004.
XX 30-APR-2004; 2004WO-US013487.
XX 01-MAY-2003; 2003US-0467171P.
XX (MUSC-) MUSC FOUND RES DEV.
XX Dong J, Rubinchik S, Moraratanadham J;
XX WPI; 2004-805118/79.
XX P-PSDB; ADU82634.
XX GENBANK; AF097365.
XX New expression vector comprising a first expression cassette with a first
PT coding region that encodes a transcriptional activating factor (TAF),
PT useful in treating cancer, AIDS, hemophilia, diabetes and asthma.
XX Disclosure; SEQ ID NO 5; 112pp; English.
XX The invention relates to an expression vector comprising a first
CC expression cassette having a first coding region that encodes a
CC transcriptional activating factor (TAF), and a second expression cassette
CC comprising a second coding region that encodes a selected polypeptide.
CC The expression vector further comprises a first expression cassette
CC having a first coding region that encodes a transcriptional activating
CC factor (TAF), the first coding region being positioned under the
CC transcriptional control of a first promoter comprising a tissue specific
CC regulatory element (TSRE), and a TAF binding site (TBS), and a second
CC expression cassette comprising a second coding region that encodes a
CC selected polypeptide, the second coding region being positioned under the
CC transcriptional control of a second promoter comprising a TSRE and a TBS,
CC that encodes a first transcriptional silencer (TSI), the third coding
CC region being positioned under the transcriptional control, a third
CC promoter comprising a TSRE and a TAB, and a fourth expression cassette
CC comprising a fourth coding region that encodes a second TSI, the fourth
CC coding region being positioned under the transcriptional control of a
CC fourth promoter that is negatively regulated by the first TSI, where the
CC first, second and third promoters are negatively regulated by the second
CC TSI. The selected polypeptide is a therapeutic polypeptide, such as an
CC anti-cancer polypeptide that is a tumor suppressor, and inducer of
CC apoptosis, and cell cycle regulator, a toxin, or an inhibitor of
CC angiogenesis, and an enzyme, a cytokine, a hormone, a tumor antigen, a
CC human antigen or a pathogen antigen. The selected polypeptide is
CC essential for vector replication, where the vector is an adenoviral
CC vector. The expression vector is useful in methods for treating cancer
CC and further comprises a selectable or screenable marker. The methods and
CC compositions of the present invention are useful in the fields of
CC molecular biology and gene therapy, particularly to the combined spatial
CC and quantitative regulation of transgene expression in eukaryotic cells,
CC and in treating cancer including breast cancer, ovarian cancer, fallopian
CC tube cancer, cervical cancer, uterine cancer, prostate cancer, testicular
CC cancer, pancreatic cancer, colon cancer, bladder cancer, liver cancer,
CC stomach cancer, lung cancer, lymphoid cancer, brain cancer, thyroid
CC cancer, head and neck cancer, skin cancer or leukemia. The cancer is a
CC recurrent cancer, a metastatic cancer or a drug resistant cancer. The
CC methods and compositions can also be used in treating cystic fibrosis,
CC AIDS, sickle cell anemia, hemophilia, diabetes, heart disease,
CC inflammatory disorders, rheumatoid arthritis, multiple sclerosis, asthma
CC and retinosis. The present sequence represents a human telomerase
CC reverse transcriptase (hTERT) gene nucleotide sequence, the promoter
CC fragment can be used in the vectors of the invention.
XX
XX Sequence 4356 BP; 829 A; 1298 C; 1254 G; 975 T; 0 U; 0 Other;

Query Match 90.4%; Score 905; DB 13; Length 4356;
Best Local Similarity 100.0%; Pred. No. 7.7e-124; Indels 0; Gaps 0;
Matches 905; Conservative 0; Mismatches 0;
QY 1 CGTCCGACCTGGAGGAGCCCTTGGGTCTCCGGATCAGGCAGCGGCAAAAGGCTGCCG 60
DB 3452 CGTCCGACCTGGAGGAGCCCTTGGGTCTCCGGATCAGGCAGCGGCAAAAGGCTGCCG 3511
QY 61 CACGACCTGTTCAGAGGCTCCACATCATATGAGCCCTCTCTGGGTATACCCACAGCCT 120
DB 3512 CACGACCTGTTCAGAGGCTCCACATCATATGAGCCCTCTCTGGGTATACCCACAGCCT 3571
QY 121 AGCCGATTCGACCTCTCCGCTGGGGCCCTCGCTGGCGCTCCTGTGACCTGGAGCGC 180
DB 3572 AGCCGATTCGACCTCTCTCCGCTGGGGCCCTCGCTGGCGCTCCTGTGACCTGGAGCGC 3631
QY 181 GAGCGCGCGCGGCGGGAAGCGCCAGACCCCGGGTCCGCCCGGAGCAGCTGCG 240
DB 3632 GAGCGCGCGCGGCGGGAAGCGCGGCCAGACCCCGGGTCCGCCCGGAGCAGCTGCG 3691
QY 241 CTGTGGGGCCAGCCCGGGCTCCAGTGGATTCCGGGCAACAGCCCGGAGCCGCGCT 300
DB 3692 CTGTGGGGCCAGCCCGGGCTCCAGTGGATTCCGGGCAACAGCCCGGAGCCGCGCT 3751
QY 301 TCCACGTGGCGAGGAGCTGGGGACCCGGGCAACCGCTCCTGCCCTTCACTTCCAGCT 360
DB 3752 TCCACGTGGCGAGGAGCTGGGGACCCGGGCAACCGCTCCTGCCCTTCACTTCCAGCT 3811
QY 361 CGGCTCTCTCCGCGCGGACCCCGCGTCCGACCCCTCCCGGGTCCCGGGCCAGCCC 420
DB 3812 CGGCTCTCTCCGCGCGGACCCCGCGTCCGACCCCTCCCGGGTCCCGGGCCAGCCC 3871
QY 421 CTTCGGGGCCCTCCAGCCCTCTCTTTCGGGGCCCGCCCTCTCTCTCGCGGCG 480
DB 3872 CTTCGGGGCCCTCCAGCCCTCTCTTTCGGGGCCCGCCCTCTCTCTCGCGGCG 3931
QY 481 CGAGTTTCAGGACGCTGGTCTCTGTGCGACGTGGGAAGCCCTGGCCCGGCGCACCC 540
DB 3932 CGAGTTTCAGGACGCTGGTCTCTGTGCGACGTGGGAAGCCCTGGCCCGGCGCACCC 3991
QY 541 CCGCATGCGCGCGCTCCCGCTGCGAGCCGTGCGCTCCCTGCTGCGAGCCACTACC 600
DB 3992 CCGCATGCGCGCGCTCCCGCTGCGAGCCGTGCGCTCCCTGCTGCGAGCCACTACC 4051
QY 601 GCAGGTGCTCGCTGGCCACAGTTGCTGGGGCCCTGGGGCCCGCAGGCTGGGGCTGG 660
DB 4052 GCAGGTGCTCGCTGGCCACAGTTGCTGGGGCCCTGGGGCCCGCAGGCTGGGGCTGG 4111
QY 661 TGCAAGCGCGGGACCCGGCGCTTTTCGCGCGCTGGTGGGCCAGTGTGTCGTGC 720
DB 4112 TGCAAGCGCGGGACCCGGCGCTTTTCGCGCGCTGGTGGGCCAGTGTGTCGTGC 4171
QY 721 CTGGGACGACGCGCGCCCGCCCGCCCTCTCTTTCGCCAGGTTGGGCTCCCCGGGG 780
DB 4172 CTGGGACGACGCGCGCCCGCCCGCCCTCTCTTTCGCCAGGTTGGGCTCCCCGGGG 4231
QY 781 TCGGGCTCGGCTGGGGTTGAGGGCGCCCGGGGGAAACAGGACATGCGGAGACGCG 840
DB 4232 TCGGGCTCGGCTGGGGTTGAGGGCGCCCGGGGGAAACAGGACATGCGGAGACGCG 4291
QY 841 CAGCGACTCAGGCGCTTCCCGCGAGGTGCTGCTGCTGAAGGAGTGTGTGGGCCCGAGT 900
DB 4292 CAGCGACTCAGGCGCTTCCCGCGAGGTGCTGCTGCTGAAGGAGTGTGTGGGCCCGAGT 4351
QY 901 GCTGC 905
DB 4352 GCTGC 4356
RESULT 12
ADV23865
ID ADV23865 standard; DNA; 4293 BP.
XX


```
AC ADV23865;
XX
XX 24-FEB-2005 (first entry)
XX
XX Human hTERT gene 5' flanking region, intron 1 and exon 1, SEQ ID 1.
XX
XX Cytostatic; Gene therapy; cancer; telomerase;
XX telomerase reverse transcriptase; hTERT; enzyme; gene; ds.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
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XX and 15"
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XX and 15"
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XX and 15"
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XX /note= "This region is responsible for full promoter
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XX /tag= l
XX /note= "This region is specifically claimed in Claims 4
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XX 09-DEC-2004.
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XX 05-JUN-2003; 2003US-00456830.
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XX 05-JUN-2003; 2003US-00456830.
XX
XX (USAS ) NASA US NAT AERO & SPACE ADMIN.
XX
XX Horikawa I, Barrett JC;
XX
XX WPI; 2005-020562/02.
XX P-PSDB; ADV23866.
XX
XX New regulatory control sequence comprising a promoter that directs
XX differential expression of an operably linked heterologous nucleic acid
XX sequence in a first cell type, useful for preparing a composition for
XX treating cancer.
XX
XX Claim 4; SEQ ID NO 1; 46pp; English.
XX
XX The present invention relates to a new regulatory control sequence (I)
XX which is useful for preparing a composition for treating cancer. (I)
XX comprises: (a) a promoter that directs differential expression of an
XX operably linked heterologous nucleic acid sequence (e.g. cytotoxins) in a
XX first cell type as compared to a second cell type, where the first cell
XX type is a telomerase-positive or a cancer cell and the second cell type
XX is a telomerase-negative or a normal somatic cell; and (b) at least one
XX exogenous E-box element linked in cis with the promoter sequence and that
XX enhances the differential expression directed by the promoter. The
XX promoter is preferably a human telomerase reverse transcriptase (hTERT)
XX promoter. hTERT is the catalytic subunit of the human telomerase complex,
XX which is responsible for the replication of telomeres. E-box elements are
XX regulatory control elements that are recognized by numerous transcription
XX factors, e.g. transcription factors from the basic helix-loop-helix
XX structural family. Differential E-box-mediated repression of hTERT gene
XX promoter activity has been discovered, where repression occurs in normal
XX cells but not in many cancer cells. By linking E-box elements in cis with
XX hTERT transcriptional regulatory sequences, the expression of heterologous
XX sequences operably linked to the hTERT transcriptional regulatory
XX sequences can be preferentially suppressed in normal cells. However, the
XX expression of such heterologous sequences is not suppressed in cancer
XX cells. The present sequence is the nucleotide sequence of the 5'-flanking
XX region, exon 1 and intron 1 of the hTERT gene, used to illustrate the
XX invention.
XX
XX Sequence 4293 BP; 817 A; 1278 C; 1234 G; 961 T; 0 U; 3 Other;
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XX Query Match 86.7%; Score 867.6; DB 14; Length 4293;
XX Best Local Similarity 99.9%; Pred. NO. 2.2e-118;
XX Matches 867; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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XX 61 CACGCACCTGTTCCAGGGCCTCCACATCATGGCCCTCCCTCGGGTTACCCACAGCT 120
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XX 121 AGGCGGATTCGACCTCTCTCCGCTGGGGCCCTCGCTGGCGTCCCTGCACCTGGAGGCGC 180
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Matches 867; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db |||||

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Db |||||

QY 1236 CAGCAGCCTGTTCCAGGCGCTCCACATCATATGCGCCCTCCCTCGGGTTACCCACAGCCT 1295

QY 121 AGGCGGATTCAGCCTCTCTCGCTGGGGCCCTCGTGGCGTCCCTGACCCCTGGAGGCG 180

Db |||||

QY 1296 AGGCGGATTCAGCCTCTCTCGCTGGGGCCCTCGTGGCGTCCCTGACCCCTGGAGGCG 1355

QY 181 GAGCGGCGCGGGGAGCGGCGCCAGAGCCCGGGTCCGCGGAGCAGCTGCG 240

Db |||||

QY 1356 GAGCGGCGCGGGGAGCGGCGCCAGAGCCCGGGTCCGCGGAGCAGCTGCG 1415

QY 241 CTGTCCGGGCGAGCGCGGCTCCAGTGATTCGCGGCGACAGAGCGCCAGGACCGCGCT 300

Db |||||

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QY 301 TCCACAGTGGCGAGGAGCTGGGAGCCCGGGACCCCGTCTGCGCCCTTCACTTCCAGCT 360

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QY 1476 TCCACAGTGGCGAGGAGCTGGGAGCCCGGGACCCCGTCTGCGCCCTTCACTTCCAGCT 1535

QY 361 CCGCTCTCTCGCGGAGCCCGCGCTGCGGAGCCCTCCCGGCTCCCGGCGCCAGGCC 420

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QY 1536 CCGCTCTCTCGCGGAGCCCGCGCTGCGGAGCCCTCCCGGCTCCCGGCGCCAGGCC 1595

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QY 1656 CAGGTTTCAGGAGCGCTGCGTCTGTCGCGACGTCGGGAGCCCTGCGCCCGCGCACCC 1715

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QY 601 GCGAGTCTCTCGCTGCGCACGTTTCGTCGCGCGCTTGGGCGCCCGAGGCTGGCGGCTGG 660

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QY 721 CTGCGGAGCAGCG 780

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QY 1896 CTGCGGAGCAGCG 1955

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QY 841 CAGGCGACTCAGGCGCTTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 868

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RESULT 14

ADV98042/c

ID ADV98042 standard; DNA; 2501 BP.

XX

XX

AC ADV98042;

XX

DT 10-MAR-2005 (first entry)

XX

DE Bisulfite treated human methylated TERT DNA (sense) Seq 134.

XX

ds; immunotherapy; DNA methylation; tumor-associated antigen; cancer; cytostatic; vaccine; TERT.

Homo sapiens.

EP1491639-A2.

29-DEC-2004.

17-JUN-2004; 2004EP-00090238.

24-JUN-2003; 2003DE-01029240.

(EPIG-) EPIGENOMICS AG.

Bichler-Mertens M, Piepenbrock C, Olek A;

WPI; 2005-050366/06.

Identifying target points for immunotherapy of tumors by analysis of methylation status of many tumor-associated antigens, also treatment, particularly vaccination, using selected antigens.

Claim 18; SEQ ID NO 134; 206pp; German.

This invention relates to a novel method for determining target points for tumor immunotherapy by taking a DNA sample from serum or other bodily fluids of a patient. Specifically, it refers to identifying the methylation status of at least one CpG island in each of 47 identified tumor-associated antigens in order to generate a methylation pattern from the results. It describes an analysis of methylation status that includes chemical treatment of DNA with a bisulfite, optionally followed by amplification, particularly methylation specific PCR (MSP) and/ or a heavy methyl technique. Accordingly, the present invention provides tumor associated antigen sequences and also the corresponding bisulfite sequences generated under differing methylation conditions. As such, the method can be used to identify targets for immunotherapy of cancers, specifically by vaccination against selected tumor-associated antigens to provide individualized immunotherapy. Furthermore, the method allows simultaneous determination of methylation status of many tumor antigens and also of other methylation-regulated cofactors important for vaccination. The pharmaceutical compositions derived thereof exhibit cytostatic activity and can be used in the development of vaccines. This polynucleotide sequence is a human tumor associated cancer-testis antigen DNA sequence that has been methylated and undergone bisulfite treatment, given in an exemplification of the invention.

Sequence 2501 BP; 504 A; 185 C; 827 G; 985 T; 0 U; 0 Other;

Query Match 62.9%; Score 629.8; DB 14; Length 2501;

Best Local Similarity 76.8%; Pred. No. 1.3e-83;

Matches 769; Conservative 0; Mismatches 232; Indels 0; Gaps 0;

QY 1 CGTCCGAGCCTGGAGGAGCCCTG3GTCTCCGGATCAGGCCAGCGCCCAAGGCTGCGCG 60

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QY 61 CAGCAGCCTGTTCCAGGCGCTCCACATCATATGCGCCCTCCCTCGGGTTACCCACAGCCT 120

Db 986 CAGCAGCCTGTTCCAGGCGCTCCACATCATATGCGCCCTCCCTCGGGTTACCCACAGCCT 927

QY 121 AGGCGGATTCAGCCTCTCTCGCTGGGGCCCTCGTGGCGTCCCTGACCCCTGGAGGCGC 180

Db 926 AAACCGATTCGACCTCTCTCGCTAAACCCCTCGTAACTCCCTACACCTTAAACAGC 867

QY 181 GAGCGCGCGCGGCGGGAAGCGCGGCCCGAGACCCCGGGTCCCGCGGAGCAGCTGGC 240

Db 866 GAAAGAGCGCGGAGCAAGAAAGAGCGAGCCAAACCCCGGATCCCGCGGAAACAACTAGC 807

QY 241 CTGTCCGGGCGAGCGCGGCTCCAGTGATTCGCGGCGACAGAGCCCGCGCGCGCGCGCT 300

Db 806 CTATCGAAACCAACCGAACTCCCAATAAATTCGCGAACAACAACGCGCCAAACCGCGCT 747


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Qy 781 TCGGGCTCCGGCTGGGCTTGAAGGGGCGCGGGGGAACCAAGGACATCGCGAGAGCAGCG 840
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Db 5513 AAACGAAACCGCGGAAACCCCGCGAAACCTTCACCACCA 5473

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GenCore version 5.1.6
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Run on: January 10, 2006, 10:08:59 ; Search time 5387 Seconds
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Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 8: gb_pt.*
- 9: gb_ro.*
- 10: gb_ats.*
- 11: gb_sy.*
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- 13: gb_vi.*
- 14: gb_htg.*
- 15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1001	100.0	4321	6	AR390473 Sequence
c 3	1001	100.0	7928	6	CS105926 Sequence
4	1001	100.0	15332	8	AF121948 Homo sapi
5	1001	100.0	15418	6	AR342806 Sequence
6	1001	100.0	15418	6	AR490112 Sequence
7	1001	100.0	15418	6	AR576878 Sequence
8	1001	100.0	15418	6	AX453025 Sequence
9	1001	100.0	15418	6	AX498409 Sequence
10	1001	100.0	15418	6	AX504952 Sequence
11	1001	100.0	92564	8	AY007685 Homo sapi
c 12	1001	100.0	161252	14	AC114955 Homo sapi
c 13	1001	100.0	202305	8	AC114291 Homo sapi
14	999.4	99.8	5491	8	AB016767 Homo sapi
15	999.4	99.8	26414	8	AF128893 Homo sapi
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19	945.8	94.5	4335	6	E36796
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21	945.8	94.5	4335	6	AX810041 Sequence
22	945.8	94.5	4335	6	BD011047 Human tel
23	926.8	92.6	4200	6	AR243331 Sequence
24	905	90.4	4356	8	AF097365 Homo sapi
25	866.4	86.6	2043	8	AF098956 Homo sapi
c 26	782	78.1	170946	14	AC117933 Papio anu
c 27	782	78.1	183506	14	AC122155 Papio anu
c 28	629.8	62.9	2501	6	CQ972391 Sequence
c 29	629.8	62.9	7928	6	CS105947 Sequence
c 30	572.2	57.2	4356	6	AX356510 Sequence
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c 38	499	49.9	1677	6	AR403725 Sequence
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43	456	45.6	2145	6	AR632801 Sequence
44	456	45.6	2645	6	BD196298 Vertebrat
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ALIGNMENTS

RESULT 1 CQ972301/c 2501 bp DNA linear PAT 05-JAN-2005
LOCUS Sequence 44 from Patent EP1491639.
DEFINITION CQ972301
ACCESSION CQ972301
VERSION CQ972301.1 GI:57163511
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Eichler-Wertens,M., Piepenbrock,C. and Olek,A.
TITLE Method of analyzing cytosin methylation status of
cancer-testis-antigens for individualised immunotherapy
JOURNAL Patent: EP 1491639-A 44 29-DEC-2004;
EpiGenomics AG (DE)
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181	Qy	GAGCGCGCGCGGGCGGGGAAAGCGGGGCCAGACCCCCGCGGTCCGCCGAGCAGCTGCG	240
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301	Qy	TCCCACTGTGGCGAGGGACTGGGGACCCGGGCAACCCGCTCTGCGCCCTTACCTTCCAGCT	360
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LOCUS	AR390473
DEFINITION	Sequence 6 from patent US 6610839.
ACCESSION	AR390473
VERSION	AR390473.1 GI:40112397
KEYWORDS	.
SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 4321)
TITLE	Morin,G.B. and Andrews,W.H.
JOURNAL	Promoter for telomerase reverse transcriptase Patent: US 6610839-A 6 26-AUG-2003;
FEATURES	Geron Corporation; Menlo Park, CA Location/Qualifiers

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ORIGIN

Query Match 100.0%; Score 1001; DB 8; Length 15332;
Best Local Similarity 100.0%; Pred. No. 3.8e-98;
Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DEFINITION Sequence 1 from patent US 6576464.
ACCESSION AR342806
VERSION AR342806.1 GI:33738009
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15418)
AUTHORS Gold,J.D. and Lebkowski,J.S.
TITLE Methods for providing differentiated stem cells
JOURNAL Patent: US 6576464-A 1 10-JUN-2003;
Geron Corporation; Menlo Park, CA
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KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15418)
AUTHORS Schiff,J.M.
TITLE Glycosyltransferase vectors for treating cancer
JOURNAL Patent: US 6713055-A 1 30-MAR-2004;
Geron Corporation, Menlo Park, CA
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Qy 1 CGTCCGACCTGGAGCGACCTCGGTCTCCGATCAGGCCAGCGCGCAAGGGTTCGCG 60
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Qy 481 CGAGTTTCAGGACGCGTGTCTGTGCGCAAGTGGGAAAGCCCTGCGCGCGCGCGCGCGCG 540
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DEFINITION Sequence 1 from patent US 6777203.
ACCESSION AR576878
VERSION AR576878.1 GI:56579198
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15418)
AUTHORS Morin,G.B., Lichtsteiner,S.P., Vasserot,A.P., Adams,R.R. and Andrews,W.H.
TITLE Telomerase promoter driving expression of therapeutic gene
JOURNAL Patent: US 6777203-A 1 17-AUG-2004;
Geron Corporation, Menlo Park, CA
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SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

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COMMENT

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Sequencing of Human Chromosome 5
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2 (bases 1 to 161252)
DOE Joint Genome Institute.
Direct Submission
Submitted (14-MAR-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: <http://www.jgi.doe.gov>

Project Information
Center Project Name: 451340
Center clone name: RPCI-11_117B23

Summary Statistics
Consensus quality: 148939 bases at least Q40
Consensus quality: 156608 bases at least Q30
Consensus quality: 158826 bases at least Q20
Estimated insert size: 175000; agarose-fp estimation
Estimated insert size: 160452; sum-of-contigs estimation
Quality coverage: 7.26 in Q20 bases; agarose-fp estimation
Quality coverage: 7.92 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 9 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

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AB0167

LOCUS

DEFINITION

ACCESS

VERSIC

KEYWORDS

SOURCE

ORGANIZATION

11

REFERENCES

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TTTT

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JOURNAL PUBMED REFERENCE AUTHORS TITLE JOURNAL	for transcriptional activation in immortalized and cancer cells Cancer Res. 59 (3), 551-557 (1999) 2 (bases 1 to 5491) Takakura,M.; Kyo,S.; Kanaya,T., Takeda,J. and Inoue,M. Submitted (04-AUG-1998) Masahiro Takakura, Kanazawa University, School of Medicine, Department of Obstetrics and Gynecology; 13-1, Takaramachi, Kanazawa, Ishikawa 920-0934, Japan (E-mail:takakura@med.kanazawa-u.ac.jp, Tel:81-76-265-2425, Fax:81-76-234-4266)
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REFERENCE 1 (bases 1 to 26414)
AUTHORS Wick, M., Zubov, D. and Hagen, G.
TITLE Genomic organization and promoter characterization of the gene encoding the human telomerase reverse transcriptase (hTERT)

JOURNAL Gene 232 (1), 97-106 (1999)
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TITLE Direct Submission
JOURNAL Submitted (16-FEB-1999) Dept. of Mol. Biol., Bayer AG Leverkusen,
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GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	999.4	99.8	44952	3	US-09-949-016-12197
7	999.4	99.8	44960	3	US-09-949-016-17583
8	999.4	99.8	51552	3	US-09-733-294A-30
9	945.8	94.5	4335	3	US-08-974-549A-6
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13	502.2	50.2	35978	3	US-09-956-335-1
14	499	49.9	1677	3	US-09-956-335-3
15	456	45.6	2135	3	US-09-502-498C-51
16	456	45.6	2135	3	US-09-502-424C-51
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; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Hayley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 633
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
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; FILING DATE: 29-Sep-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997

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APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Auserhus, Scott L.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 6:
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Db 2718 TCGGCTTCGCGCTGGGTTGAGGGCGCGCGGGGGGAAACAGCGACATGCGGAGAGCAGCG 2777
Qy 841 CAGCGACTCAGGGCGCTTCCCGCGAGGTGCTGCTGCTGAAGAGCTGGTGGGCCCGAGT 900
Db 2778 CAGCGACTCAGGGCGCTTCCCGCGAGGTGCTGCTGCTGAAGAGCTGGTGGGCCCGAGT 2837
Qy 901 GCTGCGAGGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTT 960
Db 2838 GCTGCGAGGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTT 2897
Qy 961 GAGCGGGCGCGCGGGGGCTT 1001
Db 2898 GAGCGGGCGCGCGGGGGCTT 2938
RESULT 2
US-09-783-203-1
; Sequence 1, Application US/09783203
; Patent No. 6576464
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Gold, Joseph
; APPLICANT: Lebkowski, Jane
; TITLE OF INVENTION: Tpacked stem cells
; FILE REFERENCE: 096/003
; CURRENT APPLICATION NUMBER: US/09/783,203
; CURRENT FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: 60/253,443
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/253,357
; PRIOR FILING DATE: 2000-11-27
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 15418
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-783-203-1
Query Match 100.0%; Score 1001; DB 3; Length 15418;
Best Local Similarity 100.0%; Pred. No. 3.1e-154;
Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CGTCCGACCTGGAGGAGCGCTCGGCTCCCGATCAGGCGAGCGGCAAGGGTCCGCG 60
Db 13000 CGTCCGACCTGGAGGAGCGCTCGGCTCCCGATCAGGCGAGCGGCAAGGGTCCGCG 13059
Qy 61 CAGCAGCTGTTCAGGCGCTCCACATCATATGCGCCCTCCCTCGGGTTACCCACAGCCT 120
Db 13060 CAGCAGCTGTTCAGGCGCTCCACATCATATGCGCCCTCCCTCGGGTTACCCACAGCCT 13119
Qy 121 AGCCGATTCAGCTCTCCGCTGGGGCCCTGCTGGCGTCCCTGAGGCTTACCCAGAGCG 180
Db 13120 AGCCGATTCAGCTCTCTCTCGCTGGGGCCCTGCTGGCGTCCCTGAGGCTTACCCAGAGCG 13179
Qy 181 GAGCGCGCGCGCGGGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTT 240

Db 13180 GAGCGCGCGCGCGGGAAGCGCGCCAGACCCCGCGGTCCGCGCGAGCAGCTGCG 13239
Qy 241 CTGTCCGGGGCAGCGCCGGGCTCCAGTGGATTCCGGGGCACAGACGCGCCAGGACCGGCT 300
Db 13240 CTGTCCGGGGCAGCGCCGGGCTCCAGTGGATTCCGGGGCACAGACGCGCCAGGACCGGCT 13299
Qy 301 TCCACATGCGGGAGGACTGGGGACCCCGGACCCCGTCTCTGCGCCCTTCACCTTCCAGCT 360
Db 13300 TCCACATGCGGGAGGACTGGGGACCCCGGACCCCGTCTCTGCGCCCTTCACCTTCCAGCT 13359
Qy 361 CCGGCTCTCTCGCGCGAGACCCCGGCGCGTCCGACCCCTCCGGGTCCCGGCGCGACCC 420
Db 13360 CCGGCTCTCTCGCGCGAGACCCCGGCGCGTCCGACCCCTCCGGGTCCCGGCGCGACCC 13419
Qy 421 CCTCGGGGCTCTCCAGCCCTCCGCTTCTCTTCCGGGGCCCGGCGCGTCTCTCTCGGGCG 480
Db 13420 CCTCGGGGCTCTCCAGCCCTCCGCTTCTCTTCCGGGGCCCGGCGCGTCTCTCTCGGGCG 13479
Qy 481 CGAGTTTCAGGCAAGCGCTGCGTCTCTGCGCACAGTGGGAAGCCCTGGCCCGGCGCACCC 540
Db 13480 CGAGTTTCAGGCAAGCGCTGCGTCTCTGCGCACAGTGGGAAGCCCTGGCCCGGCGCACCC 13539
Qy 541 CCGGATGCGCGCGGCTCCCGCTGCGAGCGGTGCGCTCTCTCTGCGGACGACCTACC 600
Db 13540 CCGGATGCGCGCGGCTCCCGCTGCGAGCGGTGCGCTCTCTCTGCGGACGACCTACC 13599
Qy 601 GCGAGGTGCTGCGCTGCGCACAGTTCTGCGGCGCTGGGGCCCGAGGGCTGGGGGCTGG 660
Db 13600 GCGAGGTGCTGCGCTGCGCACAGTTCTGCGGCGCTGGGGCCCGAGGGCTGGGGGCTGG 13659
Qy 661 TGACGCGCGGGGACCCCGCGGCTTTTCGCGCGGCTGGTGGGCCAGTGCTGGTGGCGTG 720
Db 13660 TGACGCGCGGGGACCCCGCGGCTTTTCGCGCGGCTGGTGGGCCAGTGCTGGTGGCGTG 13719
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Db 13720 CTGCGGACGACAGCGCGCGCCCGCGCGCTCTCTCTGCGGCGGCGCTCTCTCGGGGG 13779
Qy 781 TCGGCGTCCGCTGGGGTTGAGGGCGCGCGGGGGAAACAGCGACATGCGGAGAGCAG 840
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Qy 841 CAGCGACTCAGGCGGCTTTCCCGCGAGGTGCTCTGCTGAAAGAGCTGGTGGCGCGAGT 900
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Qy 901 GCTCAGAGGCTGTGCGAGCGCGCGGAGAAAGTGTGCGCTTTCGCGCTTTCGCGCTGCT 960
Db 13900 GCTCAGAGGCTGTGCGAGCGCGCGGAGAAAGTGTGCGCTTTCGCGCTTTCGCGCTGCT 13959
Qy 961 GGACGGGGCCCGGGGGCCCCCGGAGGCTTTCACCA 1001
Db 13960 GGACGGGGCCCGGGGGCCCCCGGAGGCTTTCACCA 14000

RESULT 3

US-09-994-427A-1
; Sequence 1, Application US/09994427A
; Patent No. 6713055
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Schiff, J. Michael
; TITLE OF INVENTION: GLYCOSYLTRANSFERASE VECTORS FOR TREATING CANCER
; FILE REFERENCE: 083,002
; CURRENT APPLICATION NUMBER: US/09/994,427A
; CURRENT FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: 60/253,395
; PRIOR FILING DATE: 2000-11-27
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1
; LENGTH: 15418
; TYPE: DNA

; ORGANISM: Homo sapiens
US-09-994-427A-1
Query Match 100.0%; Score 1001; DB 3; Length 15418;
Best Local Similarity 100.0%; Pred. No. 3.1e-154; Indels 0; Gaps 0;
Matches 1001; Conservative 0; Mismatches 0;
Qy 1 CGTCCGAGCTGAGGAGCAGCCCTGGGTCTCCGATCAGGCGCAGCGGCAAGGGTCCGCG 60
Db 13000 CGTCCGAGCTGAGGAGCAGCCCTGGGTCTCCGATCAGGCGCAGCGGCAAGGGTCCGCG 13059
Qy 61 CAGGACCTGTTCCAGGGCTTCACATCATATGGCCCTCTCTCGGGTTACCCACAGGCT 120
Db 13060 CAGGACCTGTTCCAGGGCTTCACATCATATGGCCCTCTCTCGGGTTACCCACAGGCT 13119
Qy 121 AGGCGGATTGACCTCTCTCGGTGGGGCCCTCGTGGCGTCCCTGACCTGGAGGCGC 180
Db 13120 AGGCGGATTGACCTCTCTCGGTGGGGCCCTCGTGGCGTCCCTGACCTGGAGGCGC 13179
Qy 181 GAGCGCGCGCGGCGGGAAGCGCGCCAGACCCCGGGTCCGCGGAGCAGCTGCG 240
Db 13180 GAGCGCGCGCGGCGGGAAGCGCGCCAGACCCCGGGTCCGCGGAGCAGCTGCG 13239
Qy 241 CTGTGCGGGCCAGGCGCGGCTTCCAGTGGATTTCGCGGACACAGCGCCAGGACCGGCT 300
Db 13240 CTGTGCGGGCCAGGCGCGGCTTCCAGTGGATTTCGCGGACACAGCGCCAGGACCGGCT 13299
Qy 301 TCCACATGCGGGAGGACTGGGGACCCCGGCGACCCCGTCTCTGCGCCCTTCACCTTCCAGCT 360
Db 13300 TCCACATGCGGGAGGACTGGGGACCCCGGCGACCCCGTCTCTGCGCCCTTCACCTTCCAGCT 13359
Qy 361 CCGGCTCTCTCGCGCGAGACCCCGCGCTCCGACCCCTCCGGGTCCCGGCGCGACCC 420
Db 13360 CCGGCTCTCTCGCGCGAGACCCCGCGCTCCGACCCCTCCGGGTCCCGGCGCGACCC 13419
Qy 421 CTCTCGGGCTCTCCAGCCCTCTCTCTTCTTTCGCGGCGCCCGGCGCTCTCTCGGGGG 480
Db 13420 CTCTCGGGCTCTCCAGCCCTCTCTCTTCTTTCGCGGCGCCCGGCGCTCTCTCGGGGG 13479
Qy 481 CGAGTTTCAGGCAAGCGCTGCGTCTGCGCACAGTGGGAAGCCCTGGCCCGGCGCACCC 540
Db 13480 CGAGTTTCAGGCAAGCGCTGCGTCTGCGCACAGTGGGAAGCCCTGGCCCGGCGCACCC 13539
Qy 541 CCGGATGCGCGCGGCTCCCGCTGCGAGCGGTGCGCTCTCTCTGCGGACGACCTACC 600
Db 13540 CCGGATGCGCGCGGCTCCCGCTGCGAGCGGTGCGCTCTCTCTGCGGACGACCTACC 13599
Qy 601 GCGAGGTGCTGCGCTGCGCACAGTTCTGCGGCGCTGGGGCCCGAGGGCTGGGGGCTGG 660
Db 13600 GCGAGGTGCTGCGCTGCGCACAGTTCTGCGGCGCTGGGGCCCGAGGGCTGGGGGCTGG 13659
Qy 661 TGACGCGCGGGGACCCCGCGGCTTTTCGCGCGGCTGGTGGGCCAGTGCTGGTGGCGTG 720
Db 13660 TGACGCGCGGGGACCCCGCGGCTTTTCGCGCGGCTGGTGGGCCAGTGCTGGTGGCGTG 13719
Qy 721 CTGCGGACGACAGCGCGCGCCCGCGCGCTCTCTCTGCGGCGGCGCTCTCTCGGGGG 780
Db 13720 CTGCGGACGACAGCGCGCGCCCGCGCGCTCTCTCTGCGGCGGCGCTCTCTCGGGGG 13779
Qy 781 TCGGCGTCCGCTGGGGTTGAGGGCGCGCGGGGGAAACAGCGACATGCGGAGAGCAG 840
Db 13780 TCGGCGTCCGCTGGGGTTGAGGGCGCGCGGGGGAAACAGCGACATGCGGAGAGCAG 13839
Qy 841 CAGCGACTCAGGCGGCTTTCCCGCGAGGTGCTCTGCTGAAAGAGCTGGTGGCGCGAGT 900
Db 13840 CAGCGACTCAGGCGGCTTTCCCGCGAGGTGCTCTGCTGAAAGAGCTGGTGGCGCGAGT 13899
Qy 901 GCTCAGAGGCTGTGCGAGCGCGCGGAGAAAGTGTGCGCTTTCGCGCTTTCGCGCTGCT 960
Db 13900 GCTCAGAGGCTGTGCGAGCGCGCGGAGAAAGTGTGCGCTTTCGCGCTTTCGCGCTGCT 13959
Qy 961 GGACGGGGCCCGGGGGCCCCCGGAGGCTTTCACCA 1001
Db 13960 GGACGGGGCCCGGGGGCCCCCGGAGGCTTTCACCA 14000

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Db 13960 GGACGGGCGCGGGGGCCCCCCCCCGAGGCTTCACCAACCA 14000

RESULT 4
US-09-244-438-1
; Sequence 1, Application US/09244438
; Patent No. 677203
; GENERAL INFORMATION:
; APPLICANT: Morin, Gregg B.
; APPLICANT: Lichtsteiner, Serge
; APPLICANT: Vasserot, Alain
; APPLICANT: Adams, Robert R.
; APPLICANT: Geron Corporation
; TITLE OF INVENTION: Telomerase Reverse Transcriptase Transcriptional
; FILE REFERENCE: 019/246P
; CURRENT APPLICATION NUMBER: US/09/244,438
; CURRENT FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 15418
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Human TERT promoter
US-09-244-438-1

Query Match 100.0%; Score 1001; DB 3; Length 15418;
Best Local Similarity 100.0%; Pred. No. 3.1e-154;
Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTCCGACCTGGAGGACGCTGGGTCTCCGATCAGGCGGCGGCAAGGGTCCGCG 60
Db 13000 CGTCCGACCTGGAGGACGCTGGGTCTCCGATCAGGCGGCGGCAAGGGTCCGCG 13059
Qy 61 CAGCAGCTGTCCAGGGCTCCACATCATGTGGCCCTCCTCGGGTTACCCACAGCCT 120
Db 13060 CAGCAGCTGTCCAGGGCTCCACATCATGTGGCCCTCCTCGGGTTACCCACAGCCT 13119
Qy 121 AGGCCGATTACGACTCTCTCCGCTGGGGCCCTCGCTGGCGTCCCTGACCCCTGGAGCGC 180
Db 13120 AGGCCGATTACGACTCTCTCCGCTGGGGCCCTCGCTGGCGTCCCTGACCCCTGGAGCGC 13179
Qy 181 GAGCGGCGCGGGGGAAGCGCGCCAGACCCCGGGTCCGCCCGGAGCAGCTGCG 240
Db 13180 GAGCGGCGCGGGGGAAGCGCGCCAGACCCCGGGTCCGCCCGGAGCAGCTGCG 13239
Qy 241 CTGTCCGGGCGCAGGCGGGGCTCCAGTGGATTGCGGGGCACAGACGCCCAGGACCGCGCT 300
Db 13240 CTGTCCGGGCGCAGGCGGGGCTCCAGTGGATTGCGGGGCACAGACGCCCAGGACCGCGCT 13299
Qy 301 TCCACGCTGGCGAGGACTGGGACCCCGGACCCCGTCTCGGCCCTTCCAGCT 360
Db 13300 TCCACGCTGGCGAGGACTGGGACCCCGGACCCCGTCTCGGCCCTTCCAGCT 13359
Qy 361 CCGGCTCTCTCGCGGACCCCGGCGCCCGTCCGACCCCTCCGGTCCCGGCGCAGCCC 420
Db 13360 CCGGCTCTCTCGCGGACCCCGGCGCCCGTCCGACCCCTCCGGTCCCGGCGCAGCCC 13419
Qy 421 CTTCCGGGCTCCCGAGCCCTCCCTCTCTTTCCGGGGCCCGCCCTCTCTCGGGCG 480
Db 13420 CTTCCGGGCTCCCGAGCCCTCCCTCTCTTTCCGGGGCCCGCCCTCTCTCGGGCG 13479
Qy 481 CGAGTTTCAGGACGCTCGGTCTCTGTGGCGCAGTGGGAAGCCCTGGCCCGGCGCACCC 540
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Qy 541 CCGGATGCCCGGCTCCCGCTGCGGAGCGCTGCGCTCTCTGCTGGGAGCCTAC 600
Db 13540 CCGGATGCCCGGCTCCCGCTGCGGAGCGCTGCGCTCTCTGCTGGGAGCCTAC 13599
Qy 601 GCGAGGTGCTGCCCTGGCCACAGTTCTGTGGGCGCTGGGGGCCCGCAGGGCTGGGGCTGG 660
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Qy 721 CTTGGAGCGCACCGCGCGCCCGCGCGCCCTCTTCCCGCCAGGTGGGCTCTCCCGGGG 780
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Qy 841 CAGCGACTCAGGGCGCTTCCCGCGAGGTGTCTGCTGAAAGAGTGTGTGGGCCGAGT 900
Db 13840 CAGCGACTCAGGGCGCTTCCCGCGAGGTGTCTGCTGAAAGAGTGTGTGGGCCGAGT 13899
Qy 901 GCTGCAGAGGCTGTGCGAGCGCGCGGGAAGACGTGCTTGGCTTCCGCTTCCGCTGCTGCT 960
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RESULT 5
US-09-995-419A-1
; Sequence 1, Application US/09995419A
; Patent No. 6921665
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: McWhir, Jim
; APPLICANT: Gold, Joseph D.
; APPLICANT: Schiff, J. Michael
; TITLE OF INVENTION: 096,004 - SeqList
; FILE REFERENCE: 096,004 - SeqList
; CURRENT APPLICATION NUMBER: US/09/995,419A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 60/253,357
; PRIOR FILING DATE: 2000-11-27
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 15418
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-995-419A-1

Query Match 100.0%; Score 1001; DB 3; Length 15418;
Best Local Similarity 100.0%; Pred. No. 3.1e-154;
Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTCCGACCTGGAGGACGCTGGGTCTCCGATCAGGCGGCGGCAAGGGTCCGCG 60
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Qy 61 CAGCAGCTGTTCACAGGGCTCCACATCATGTGGCCCTCCTCGGGTTACCCACAGCCT 120
Db 13060 CAGCAGCTGTTCACAGGGCTCCACATCATGTGGCCCTCCTCGGGTTACCCACAGCCT 13119
Qy 121 AGGCCGATTACGACTCTCTCCGCTGGGGCCCTCGCTGGCGTCCCTGACCCCTGGAGCGC 180
Db 13120 AGGCCGATTACGACTCTCTCCGCTGGGGCCCTCGCTGGCGTCCCTGACCCCTGGAGCGC 13179
Qy 181 GAGCGGCGCGGGGGAAGCGCGCCAGACCCCGGGTCCGCCCGGAGCAGCTGCG 240
Db 13180 GAGCGGCGCGGGGGAAGCGCGCCAGACCCCGGGTCCGCCCGGAGCAGCTGCG 13239
Qy 241 CTGTCCGGGCGCAGGCGGGGCTCCAGTGGATTGCGGGGCACAGACGCCCAGGACCGCGCT 300
Db 13240 CTGTCCGGGCGCAGGCGGGGCTCCAGTGGATTGCGGGGCACAGACGCCCAGGACCGCGCT 13299
Qy 301 TCCACGCTGGCGAGGACTGGGACCCCGGACCCCGTCTCGGCCCTTCCAGCT 360
Db 13300 TCCACGCTGGCGAGGACTGGGACCCCGGACCCCGTCTCGGCCCTTCCAGCT 13359
Qy 361 CCGGCTCTCTCGCGGACCCCGGCGCCCGTCCGACCCCTCCGGTCCCGGCGCAGCCC 420
Db 13360 CCGGCTCTCTCGCGGACCCCGGCGCCCGTCCGACCCCTCCGGTCCCGGCGCAGCCC 13419
Qy 421 CTTCCGGGCTCCCGAGCCCTCCCTCTCTTTCCGGGGCCCGCCCTCTCTCGGGCG 480
Db 13420 CTTCCGGGCTCCCGAGCCCTCCCTCTCTTTCCGGGGCCCGCCCTCTCTCGGGCG 13479
Qy 481 CGAGTTTCAGGACGCTCGGTCTCTGTGGCGCAGTGGGAAGCCCTGGCCCGGCGCACCC 540
Db 13480 CGAGTTTCAGGACGCTCGGTCTCTGTGGCGCAGTGGGAAGCCCTGGCCCGGCGCACCC 13539
Qy 541 CCGGATGCCCGGCTCCCGCTGCGGAGCGCTGCGCTCTCTGCTGGGAGCCTAC 600
Db 13540 CCGGATGCCCGGCTCCCGCTGCGGAGCGCTGCGCTCTCTGCTGGGAGCCTAC 13599
Qy 601 GCGAGGTGCTGCCCTGGCCACAGTTCTGTGGGCGCTGGGGGCCCGCAGGGCTGGGGCTGG 660
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Db 13240 CTGTGGGGCCAGGCGCGGGCTCCAGTGGATTGCGGGGACACAGACGCCCGCGGCT 13299
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Db 13300 TCCACAGTGGCGGAGGAGCTGGGAGACCGGGACACCGCTGCTGCGCCCTTCACTTCCAGCT 13359
Qy 361 CCGCTCTCTCCGCGCGGACCCCGCGCTCCCGGCTCCCGGAGTCCCGGCGCCAGGCC 420
Db 13360 CCGCTCTCTCCGCGCGGACCCCGCGCTCCCGGCTCCCGGAGTCCCGGCGCCAGGCC 13419
Qy 421 CTTCCGGGCTCTCCAGGCTCTCCCTTCTTCCGCGGCTCCCGGCTCTCTCCGCGGCT 480
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Qy 481 CGAGTTTCAGGACAGCGCTGCTGCTGCTGCGACGTCGAGGAGCTGCGCCCGGCGCACCC 540
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Db 13780 TCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 13839
Qy 841 CAGGAGTCTAGGAGCTTCCCGCTCCCGGCTCCCGGAGTGGGCTCCCGGCTCCCGGCTG 900
Db 13840 CAGGAGTCTAGGAGCTTCCCGCTCCCGGAGTGGGCTCCCGGCTCCCGGCTCCCGGCTG 13899
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Qy 961 GAGCGGGGCGCGGCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1001
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RESULT 6
US-09-949-016-12197
; Sequence 12197; Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12197
; LENGTH: 44952
; TYPE: DNA
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; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(44952)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12197

Query Match          99.8%; Score 999.4; DB 3; Length 44952;
Best Local Similarity 99.9%; Pred. No. 5.3e-154;
Matches 1000; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGTCCGAGCTTGGAGGAGCGCTTGGGTCTCCGATCAGGCGCAGCGGCGCAAAAGGCTGCGCG 60
Db 1511 CGTCCGAGCTTGGAGGAGCGCTTGGGTCTCCGATCAGGCGCAGCGGCGCAAAAGGCTGCGCG 1570
Qy 61 CAGCAGCTGTTCCAGGGCTCCACATCATATGCGCCCTCCCTCGGTTTACCCACAGCT 120
Db 1571 CAGCAGCTGTTCCAGGGCTCCACATCATATGCGCCCTCCCTCGGTTTACCCACAGCT 1630
Qy 121 AGGCGGATTCGACCTCTCTCCGCTGGGGCTCCGCTGCGCTCCCTGCACTTGGAGCGC 180
Db 1631 AGGCGGATTCGACCTCTCTCCGCTGGGGCTCCGCTGCGCTCCCTGCACTTGGAGCGC 1690
Qy 181 GAGCGGCGCGCGCGGAGAGCGGCGCCAGACCCCGGGTCCCGCGGAGCGAGCTGCG 240
Db 1691 GAGCGGCGCGCGCGGAGAGCGGCGCCAGACCCCGGGTCCCGCGGAGCGAGCTGCG 1750
Qy 241 CTGTCCGGGCGCAGCGCGGCTCCAGTGGATTTCGGGGCAGAGCGCCAGACCGCGCT 300
Db 1751 CTGTCCGGGCGCAGCGCGGCTCCAGTGGATTTCGGGGCAGAGCGCCAGACCGCGCT 1810
Qy 301 TCCACAGTGGCGGAGGAGCTTGGGAGACCGGCGACCCCGTCTGCGCCCTTCACTTCCAGCT 360
Db 1811 CCCCAGTGGCGGAGGAGCTTGGGAGACCGGCGACCCCGTCTGCGCCCTTCACTTCCAGCT 1870
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Qy 421 CTTCCGGGCTCCAGCGCTTCCCTTCCGCGGCGCCCGCTCTCTCTCGCGGCTCCCTCTCG 480
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Db 2111 CCGAGTGTCTCCCGCTGGGCTTGGTGGCGGCTGGGGCGCCAGGGCTGGCGGCTGG 2170
Qy 661 TCGAGCGCGGAGACCCCGGCTTTCGCGGCTTTCGCGGCTTTCGCGGCTTTCGCGGCTTTC 720
Db 2171 TCGAGCGCGGAGACCCCGGCTTTCGCGGCTTTCGCGGCTTTCGCGGCTTTCGCGGCTTTC 2230
Qy 721 CTTGGAGCGACGCGCGCTCCCGCTCCCGGCTCCCTTCCCGGAGTGGGCTTCCCGGCT 780
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Qy 781 TCGGCTCCCGCTGGGTTGAGGGCGCGCGGGGGGAGACAGGAGCATGCGGAGAGCGG 840
Db 2291 TCGGCTCCCGCTGGGTTGAGGGCGCGCGGGGGGAGACAGGAGCATGCGGAGAGCGG 2350
Qy 841 CAGGAGCTCAGGGCGCTTCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
Db 2351 CAGGAGCTCAGGGCGCTTCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2410
Qy 901 GCTCAGAGGCTGTGCGAGCGCGCGCGGAGAAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
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Db 2411 GCTGCAGAGGCTGTGTCGAGCGCGCGGAGAACGTCGTGGCCCTTCGGCTTCGGCGCTGCT 2470
Qy 961 GGACGGGGCGCGGGGGCCCCCGGAGGCTTTCACACCA 1001
Db 2471 GGACGGGGCGCGGGGGCCCCCGGAGGCTTTCACACCA 2511
RESULT 7
US-09-949-016-17583
; Sequence 17583, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17583
; LENGTH: 44960
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(44960)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17583

Query Match 99.8%; Score 999.4; DB 3; Length 44960;
Best Local Similarity 99.9%; Pred. No. 5.3e-154;
Matches 1000; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy 121 AGGCGGATTCAGCTCTCTCGCTGGGGCCCTCGCTGGCGTCCCTGCACCTGGGAGGC 180
Db 1631 AGGCGGATTCAGCTCTCTCGCTGGGGCCCTCGCTGGCGTCCCTGCACCTGGGAGGC 1690
Qy 181 GAGCGGCGCGCGGGGAGCGCGGCCAGAGCCCGGGTCCCGCGGAGCAGCTGCG 240
Db 1691 GAGCGGCGCGCGGGGAGCGCGGCCAGAGCCCGGGTCCCGCGGAGCAGCTGCG 1750
Qy 241 CTGTCCGGGCGAGCGCGGGCTCCAGTGATTCGCGGCGACAGCGCCAGGACCGGCT 300
Db 1751 CTGTCCGGGCGAGCGCGGGCTCCAGTGATTCGCGGCGACAGCGCCAGGACCGGCT 1810
Qy 301 TCCACGTGGCGGAGGACTGGGAGCCGGGACCCGCTCGCTGGCCCTTCCAGCT 360
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Qy 361 CCGGCTCTCTCCGCGGAGCCCGCGCTCCCGACCCCTCCCGGGTCCCGGGCCAGGCC 420
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Qy 421 CCTCCGGGCTCCCGAGCCCTCCCTTCCTTCGCGGGCCCGCCCTCTCTCGCGGG 480
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Db 1991 CGAGTTTCAGCAGCGGCTCGCTCTCTGTCGACGTCGGAGCCCTTGGCCCGGCCACC 2050
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Qy 781 TCGCGCTCCGCTGGGGTTGAGGGCGGCGCGGGGGGGAACCGACATGCGGAGGAGCAGCG 840
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; Sequence 30, Application US/09733294A
; Patent No. 6492171
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: William Gaarde
; APPLICANT: Susan M. Freier
; APPLICANT: Edward V. Wanciewicz
; TITLE OF INVENTION: ANTISENSE MODULATION OF TERT EXPRESSION
; FILE REFERENCE: ISPH-0527
; CURRENT APPLICATION NUMBER: US/09/733,294A
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 09/572,423
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 108
; SEQ ID NO 30
; LENGTH: 51552
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: exon
; LOCATION: (1)...(11492)
; OTHER INFORMATION: exon 1
; NAME/KEY: intron
; LOCATION: (11493)...(11596)
; OTHER INFORMATION: intron 1
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; LOCATION: (11597)...(12950)
; OTHER INFORMATION: exon 2
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; LOCATION: (21567)...(21762)
; OTHER INFORMATION: exon 3
; NAME/KEY: intron

; LOCATION: (21763)...(23851)
; OTHER INFORMATION: intron 3
; NAME/KEY: exon
; LOCATION: (23852)...(24032)
; OTHER INFORMATION: exon 4
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; LOCATION: (31273)...(31358)
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; LOCATION: (31359)...(33843)
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; NAME/KEY: unsure
; LOCATION: 31450
; OTHER INFORMATION: unknown
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; LOCATION: (33844)...(33957)
; OTHER INFORMATION: exon 9
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; OTHER INFORMATION: intron 9
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; LOCATION: (35942)...(36013)
; OTHER INFORMATION: exon 10
; NAME/KEY: intron
; LOCATION: (36014)...(37884)
; OTHER INFORMATION: intron 10
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; OTHER INFORMATION: exon 11
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; LOCATION: (38074)...(41874)
; OTHER INFORMATION: intron 11
; NAME/KEY: exon
; LOCATION: (41875)...(42001)
; OTHER INFORMATION: exon 12
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; LOCATION: (42002)...(42881)
; OTHER INFORMATION: intron 12
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; LOCATION: (42882)...(42943)
; OTHER INFORMATION: exon 13
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; LOCATION: (42944)...(46129)
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; LOCATION: (46130)...(46254)
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; LOCATION: (47036)...(47173)

; OTHER INFORMATION: exon 15
; NAME/KEY: intron
; LOCATION: (47174)...(47709)
; OTHER INFORMATION: intron 15
; NAME/KEY: exon
; LOCATION: (47710)...(50544)
; OTHER INFORMATION: exon 16
US-09-733-294A-30

Query Match 99.8%; Score 999.4; DB 3; Length 51552;
Best Local Similarity 99.9%; Pred. No. 5.2e-154;
Matches 1000; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 10789 CACGACCTGTTCCAGGGCTCCACATCATATGGCCCTCCCTCGGGTTACCCACAGCT 10848
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Qy 601 GCGAGGTGCTGCGCTGGCCACGTTTCGTCGCGCGCTGGGGCCCGGAGGCTGGCGGCTGG 660
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Qy 661 TGCAGCGCGGGAACCCCGCGGCTTTCGCGGCTGGTGGCCAGTGCCTGTGTGTGCTGTC 720
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Qy 721 CCTGGGACGACGGCGCGCCCGCGCGCTCCCTCCCTCCGCGAGGTGGGCTCCCGCGGG 780
Db 11449 CCTGGGACGACGGCGCGCCCGCGCGCTCCCTCCCTCCGCGAGGTGGGCTCCCGCGGG 11508
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Db 11509 TCGGCTCCGCTGGGGTTGAGGGCGCGCGGGGGAACACAGCAATCGGAGAGCAGCG 11568
Qy 841 CAGCGACTCAGGGCGCTTCCCGCGAGTGTCTGTCTGCTGAAGGAGCTGTGTGCGCCGAGT 900
Db 11569 CAGCGACTCAGGGCGCTTCCCGCGAGTGTCTGTCTGCTGAAGGAGCTGTGTGCGCCGAGT 11628

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597	Qy	TACCGGAGGTGCTGCCGCTGGCCACGTTCTGTGCGGCGCTTGGGGCCCCCAGGAGCTGCGG	656
2547	Db	TACCGGAGGTGCTGCCGCTGGCCACGTTCTGTGCGGCGCTTGGGGCCCCCAGGAGCTGCGG	2606
657	Qy	CTGTGTGACGCGCGGGGACCCGGCGGCTTTCCGCGCGCTGTGTGCGCCAGTGCCTTGTGTGC	716
2607	Db	CTGTGTGACGCGCGGGGACCCGGCGGCTTTCCGCGCGCTGTGTGCGCCAGTGCCTTGTGTGC	2666
717	Qy	GTGCGCTGGAGACGACGGCGCGCCCCCGCGCCCTCTCTTCGCGCAGTGGGCGCTCCCC	776
2667	Db	GTGCGCTGGAGACGACGGCGCGCCCCCGCGCCCTCTCTTCGCGCAGTGGGCGCTCCCC	2726
777	Qy	GGGCTCGGCGCTCGGCTTGGGCTTGAAGGCGCGCGGGGGAAACACAGCACATGCGCGAGAGC	836
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837	Qy	AGCGCAGGCGACTCAGGGCGCTTCCCGCGCAGTGTCTCTGCTGAAGGAGCTGTTGGCCCC	896
2787	Db	AGCGCAGGCGACTCAGGGCGCTTCCCGCGCAGTGTCTCTGCTGAAGGAGCTGTTGGCCCC	2846
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2847	Db	GAGTGTGACAGAGCTGTGCGAGCGCGCGCAAGAACGTGTGGCTTTCGCGTTCGCGC	2906
957	Qy	TGCTGGACGGGGCCCCCGGGGGCCCCCCCCCGAGGCGCTTTCACACCA	1001
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RESULT 11

US-08-912-951-6
; Sequence 6, Application US/08912951
; Patent No. 6475789
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
; THERAPEUTIC METHODS
; NUMBER OF SEQUENCES: 335
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/912,951
; FILING DATE: 14-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:


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Qy 481 CGAGTTTCAGGACGCGTGGTCTGCG 507
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RESULT 14
US-09-556-335-3/c
; Sequence 3, Application US/09956335
; Patent No. 6627190
; GENERAL INFORMATION:
; APPLICANT: WOLD, William
; APPLICANT: TOTH, Karoly
; APPLICANT: KUPPASWAMI, Mohan
; APPLICANT: DORONIN, Konstantin
; TITLE OF INVENTION: RECOMBINANT ADENOVIRUS VECTORS THAT ARE
; TITLE OF INVENTION: REPLICATION-COMPETENT IN TERT-EXPRESSING CELLS
; FILE REFERENCE: 16153-8394
; CURRENT APPLICATION NUMBER: US/09/956,335
; CURRENT FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1677
; TYPE: DNA
; ORGANISM: Adenovirus
; US-09-556-335-3

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Best Local Similarity 100.0%; Pred. No. 9.1e-73; Mismatches 0; Indels 0; Gaps 0;
Matches 499; Conservative 0;

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Qy 121 AGCCGGAATTGACCTCTCTCGCTGGGCGCTCTGCTGGCGCTCCCTGACCTGGGAGCGC 180
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RESULT 15
US-09-502-498C-51
; Sequence 51, Application US/09502498C
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; Patent No. 6846662
; GENERAL INFORMATION:
; APPLICANT: Kilian, Andrzej
; APPLICANT: Bowtell, David
; TITLE OF INVENTION: VERTEBRATE TELOMERASE GENES AND PROTEINS AND USBS
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 407C2
; CURRENT APPLICATION NUMBER: US/09/502,498C
; CURRENT FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 51
; LENGTH: 2135
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (1871)..(1873)
; OTHER INFORMATION: Wherein N is A, C, G or T
; FEATURE:
; OTHER INFORMATION: Truncated Telomerase (ver. 2); with
; OTHER INFORMATION: Intron Y
; US-09-502-498C-51

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Best Local Similarity 100.0%; Pred. No. 8.5e-66; Mismatches 0; Indels 0; Gaps 0;
Matches 456; Conservative 0;

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 10, 2006, 10:37:31 ; Search time 949.333 Seconds
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1001	100.0	15418	3	US-09-783-203-1
3	1001	100.0	15418	3	US-09-994-427A-1
4	1001	100.0	15418	3	US-09-995-419A-1
5	1001	100.0	15418	5	US-10-141-220-1
6	1001	100.0	15418	5	US-10-023-969-1
7	1001	100.0	15418	5	US-10-208-447-1
8	1001	100.0	15418	7	US-10-674-836-1
9	1001	100.0	15418	7	US-10-811-012-1
10	988.6	98.8	4293	8	US-10-456-830-1
11	972.8	97.2	5126	8	US-10-840-455-1
12	972.8	97.2	11276	8	US-10-840-455-3
13	972.8	97.2	26414	8	US-10-840-455-43
14	972.8	97.2	51552	3	US-09-733-294A-30
15	930.8	93.0	4335	8	US-10-877-124-6
16	930.8	93.0	4335	8	US-10-877-022-6
17	930.8	93.0	4335	8	US-10-877-146-6
18	677.8	67.7	35971	3	US-09-956-335-2
19	677.8	67.7	35978	3	US-09-956-335-1
20	676	67.5	1677	3	US-09-956-335-3
21	643.2	64.3	4356	7	US-10-240-589C-144
22	636	63.5	4356	7	US-10-240-589C-143
23	497	49.7	497	7	US-10-674-836-22

24	240	24.0	3186778	5	US-10-027-632-174961	Sequence 174961,
25	240	24.0	3186778	6	US-10-027-632-174961	Sequence 174961,
26	229.8	23.0	4200	5	US-10-044-692-6	Sequence 6, Appli
27	229.8	23.0	4200	5	US-10-044-539-6	Sequence 6, Appli
28	136.4	13.6	158980	8	US-10-422-522-32	Sequence 32, Appli
29	134.2	13.4	18596	3	US-09-880-107-1590	Sequence 119, Ap
30	134.2	13.4	18596	3	US-09-967-768A-119	Sequence 124, App
31	134.2	13.4	18596	3	US-09-954-531-124	Sequence 140, App
32	134.2	13.4	18596	3	US-09-954-531-348	Sequence 140, App
33	134.2	13.4	18596	8	US-10-629-313-140	Sequence 1191, Ap
34	134.2	13.4	18596	9	US-10-843-641A-1191	Sequence 1415, Ap
35	134.2	13.4	18596	9	US-10-843-641A-1415	Sequence 6264, Ap
36	134.2	13.4	18596	9	US-10-843-641A-6264	Sequence 822099,
C 37	133.8	13.3	591	4	US-09-925-065A-822099	Sequence 566446,
C 38	132.8	13.3	584	4	US-09-925-065A-566446	Sequence 484, App
C 39	132.8	13.3	196686	5	US-10-087-192-484	Sequence 566447,
C 40	132.8	13.2	584	4	US-09-925-065A-566447	Sequence 740337,
C 41	132.2	13.2	565	4	US-09-925-065A-740337	Sequence 740801,
C 42	132.2	13.2	567	4	US-09-925-065A-740801	Sequence 682612,
C 43	132.2	13.2	594	4	US-09-925-065A-682612	Sequence 682613,
C 44	132.2	13.2	594	4	US-09-925-065A-682613	Sequence 4, Appli
C 45	132.2	13.2	24295	7	US-10-317-277A-4	

ALIGNMENTS

RESULT 1
US-10-325-810-6
; Sequence 6, Application US/10325810
; Publication No. US20030204069A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; ; Lingner, Joachim
; ; Nakamura, Toru
; ; Chapman, Karen B.
; ; Morin, Gregg B.
; ; Harley, Calvin B.
; ; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 633
; CORRESPONDENCE ADDRESS:
; ADDRESS: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/325,810
; FILING DATE: 20-Dec-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/402,181
; FILING DATE: 29-Sep-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951

;; FILING DATE: 14-AUG-1997
;; APPLICATION NUMBER: US 08/915,503
;; FILING DATE: 14-AUG-1997
;; APPLICATION NUMBER: WO PCT/US97/17885
;; FILING DATE: 01-OCT-1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Aussenhus, Scott L.
;; REGISTRATION NUMBER: 42,271
;; REFERENCE/DOCKET NUMBER: 015389-002620US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 576-0200
;; TELEFAX: (415) 576-0300
;; INFORMATION FOR SEQ ID NO: 6:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 4321 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; FEATURE:
;; NAME/KEY: -
;; LOCATION: 1..4321
;; OTHER INFORMATION: /note= "genomic DNA insert of pGRN144"

;; NAME/KEY: intron
;; LOCATION: 2702..2804
;; OTHER INFORMATION: /note= "intron 1"
;; FEATURE:
;; NAME/KEY: intron
;; LOCATION: 4160..4313
;; OTHER INFORMATION: /note= "intron 2"

;; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-325-810-6

Query Match 100.0%; Score 1001; DB 6; Length 4321;
Best Local Similarity 100.0%; Pred. No. 6.9e-295;
Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGCTGGGATTACAGGACCCGCGACCATGCGCAGCTAATTTTGTATTTTGTATTTAGTAGAGA 60
Db 438 GGCTGGGATTACAGGACCCGCGACCATGCGCAGCTAATTTTGTATTTTGTATTTAGTAGAGA 497

Qy 61 CGGGGGTGGGGTGGGGTTCACCATGTTGGCCAGCTGCTCGAATCTTGTGACCTCAGA 120
Db 498 CGGGGGTGGGGTGGGGTTCACCATGTTGGCCAGCTGCTCGAATCTTGTGACCTCAGA 557

Qy 121 TGATCCACCTGCTCTGCTCTCTAAAGTGTGGGATTACAGGTGTGAGCCACCATGCCCA 180
Db 558 TGATCCACCTGCTCTGCTCTCTAAAGTGTGGGATTACAGGTGTGAGCCACCATGCCCA 617

Qy 181 GCTCAGAAATTACTCTGTTTGTAGAAACATCTGGGTCTGAGGTAGGAAGCTCACCCCACTCA 240
Db 618 GCTCAGAAATTACTCTGTTTGTAGAAACATCTGGGTCTGAGGTAGGAAGCTCACCCCACTCA 677

Qy 241 AGTGTCTGGTGTGTTTAAAGCAATGATAGAAATTTTATTTTGTGTTAGAACACTCTTGA 300
Db 678 AGTGTCTGGTGTGTTTAAAGCAATGATAGAAATTTTATTTTGTGTTAGAACACTCTTGA 737

Qy 301 TGTTTTACACTGTGATGACTAAGACATCATCAGCTTTTCAAAGACACACTAATGACACC 360
Db 738 TGTTTTACACTGTGATGACTAAGACATCATCAGCTTTTCAAAGACACACTAATGACACC 797

Qy 361 ATAATACATGGGGTCTCTTCTGGGTATCAGCGATCTTCAATGAAATGCGGGAGGGTTTCC 420
Db 798 ATAATACATGGGGTCTCTTCTGGGTATCAGCGATCTTCAATGAAATGCGGGAGGGTTTCC 857

Qy 421 TCGCCATGCACATGGTGTAAATTAATCTCAGATAATCTCTGCTTCCATTTCTTCTTCC 480
Db 858 TCGCCATGCACATGGTGTAAATTAATCTCAGATAATCTCTGCTTCCATTTCTTCTTCC 917

Qy 481 CCTCTTTTAAATTTGTTTTCTATGTTGGCTTCTCTGCAGAGAACACAGGTGTAAGCTACA 540
Db 918 CCTCTTTTAAATTTGTTTTCTATGTTGGCTTCTCTGCAGAGAACACAGGTGTAAGCTACA 977

Qy 541 ACTTAACCTTTTGTGGAAACAAATTTTCCAAACCGCCCTTTGCCCTAGTGGCAGAGACAA 600
Db 978 ACTTAACCTTTTGTGGAAACAAATTTTCCAAACCGCCCTTTGCCCTAGTGGCAGAGACAA 1037

Qy 601 TTCACAAACACAGCCCTTTTAAAGGGCTTAAAGGATCACTAAGGGGATTTCTAGAAAGAGCG 660
Db 1038 TTCACAAACACAGCCCTTTTAAAGGGCTTAAAGGATCACTAAGGGGATTTCTAGAAAGAGCG 1097

Qy 661 ACCCGTAATCTTAAGTATTTTACAAGACGAGGCTAAACCTCAGCGAGCGTGCAGCCGAGG 720
Db 1098 ACCCGTAATCTTAAGTATTTTACAAGACGAGGCTAAACCTCAGCGAGCGTGCAGCCGAGG 1157

Qy 721 GAGGGTGCAGGGCTGTTCAAAATGCTAGCTCCATAAATAAAGCAATTTTCTCCGGCAGTT 780
Db 1158 GAGGGTGCAGGGCTGTTCAAAATGCTAGCTCCATAAATAAAGCAATTTTCTCCGGCAGTT 1217

Qy 781 TCTGAAAGTAGGAAAGGTTACATTTAAAGGTTGCGTTTGTAGCAATTTTCAAGTGTTCGCGA 840
Db 1218 TCTGAAAGTAGGAAAGGTTACATTTAAAGGTTGCGTTTGTAGCAATTTTCAAGTGTTCGCGA 1277

Qy 841 CCTCAGCTACAGCATCCCTGCAAGGCTCGGGAGACCCAGAAAGTTTCTCGCCCTTAGAT 900
Db 1278 CCTCAGCTACAGCATCCCTGCAAGGCTCGGGAGACCCAGAAAGTTTCTCGCCCTTAGAT 1337

Qy 901 CCAAACTTGAGCAACCCGAGTCTGGATTCCTGGGAAGTCTCAGCTGTCTGCGGTTGT 960
Db 1338 CCAAACTTGAGCAACCCGAGTCTGGATTCCTGGGAAGTCTCAGCTGTCTGCGGTTGT 1397

Qy 961 GCCGGGGCCCCAGTCTGAGAGGGACCCAGTGGCCGTGTGGC 1001
Db 1398 GCCGGGGCCCCAGTCTGAGAGGGACCCAGTGGCCGTGTGGC 1438

RESULT 2

US-09-783-203-1
; Sequence 1, Application US/09783203
; Patent No. US20020098582A1
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Gold, Joseph
; APPLICANT: Lebkowski, Jane
; TITLE OF INVENTION: Tpacked stem cells
; FILE REFERENCE: 096/003
; CURRENT APPLICATION NUMBER: US/09/783,203
; CURRENT FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: 60/253,443
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/253,357
; PRIOR FILING DATE: 2000-11-27
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 15418
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-783-203-1

Query Match 100.0%; Score 1001; DB 3; Length 15418;
Best Local Similarity 100.0%; Pred. No. 1.4e-294;
Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGCTGGGATTACAGGACCCGCGACCATGCGCAGCTAATTTTGTATTTTGTATTTAGTAGAGA 60
Db 11500 GGCTGGGATTACAGGACCCGCGACCATGCGCAGCTAATTTTGTATTTTGTATTTAGTAGAGA 11559

Qy 61 CGGGGGTGGGGTGGGGTTCACCATGTTGGCCAGCTGCTCGAATCTTGTGACCTCAGA 120
Db 11560 CGGGGGTGGGGTGGGGTTCACCATGTTGGCCAGCTGCTCGAATCTTGTGACCTCAGA 11619

Qy 121 TGATCCACCTGCTCTGCTCTCTAAAGTGTGCGGATTTACAGGTGTGAGCCACCATGCCCA 180
Db 11620 TGATCCACCTGCTCTGCTCTCTAAAGTGTGCGGATTTACAGGTGTGAGCCACCATGCCCA 11679

QY	181	GCTCAGAAATTACTCTGTTTTAGAAA	CATCTGGGCTGAGGTAGGAAGCTC	CACCCCACTCA	240	
Db	11680	GCTCAGAAATTACTCTGTTTTAGAAA	CATCTGGGCTGAGGTAGGAAGCTC	CACCCCACTCA	11739	
QY	241	AGTCTTGCGTGGTTTAAAGCCAA	TGATAGAAATTTTTTTTATCTTGTTAGAA	CACCTCTTGA	300	
Db	11740	AGTCTTGCGTGGTTTAAAGCCAA	TGATAGAAATTTTTTTTATCTTGTTAGAA	CACCTCTTGA	11799	
QY	301	TGTTTTACACTGTGATGAC	TAAAGACATCATCAGCTTTTCAAAGAC	CACACTAATGCA	360	
Db	11800	TGTTTTACACTGTGATGAC	TAAAGACATCATCAGCTTTTCAAAGAC	CACACTAATGCA	11859	
QY	361	ATAATACTGGGCTGCTTTCTGGG	TATCAGCGATCTTTCAATGAATCGCGGAGCG	GTTC	420	
Db	11860	ATAATACTGGGCTGCTTTCTGGG	TATCAGCGATCTTTCAATGAATCGCGGAGCG	GTTC	11919	
QY	421	TGCGCATGCA	CATGGTGTTAAATTA	CTCCAGACA	TAATCTTCTGCTTCCATTTCTCTCTTC	480
Db	11920	TGCGCATGCA	CATGGTGTTAAATTA	CTCCAGACA	TAATCTTCTGCTTCCATTTCTCTCTTC	11979
QY	481	CCTCTTTTAAATTTGCTGTTTTCT	ATGTTGGCTTCTCTGCAGAGAA	CCAGTGTGA	AGCTACA	540
Db	11980	CCTCTTTTAAATTTGCTGTTTTCT	ATGTTGGCTTCTCTGCAGAGAA	CCAGTGTGA	AGCTACA	12039
QY	541	ACTTAACTTTTGTGGAA	CAAAATTTTCCAAACCGCCCTTTG	CCCTAGTGGCAGAGACA	CAA	600
Db	12040	ACTTAACTTTTGTGGAA	CAAAATTTTCCAAACCGCCCTTTG	CCCTAGTGGCAGAGACA	CAA	12099
QY	601	TTCAAAACACAGCCCTTTTAA	AAAGGCTTAGGATCACATAAGGGGAT	TTCTAGAGAGCG	660	
Db	12100	TTCAAAACACAGCCCTTTTAA	AAAGGCTTAGGATCACATAAGGGGAT	TTCTAGAGAGCG	12159	
QY	661	ACCCGTAATCCTAAGTATTTA	CAAGACGAGGCTTAACCTCCAGCAGCGTGA	CAGCCCA	720	
Db	12160	ACCCGTAATCCTAAGTATTTA	CAAGACGAGGCTTAACCTCCAGCAGCGTGA	CAGCCCA	12219	
QY	721	GAGGGTCGGAGGCTGTG	CAAAATCTAGCTCCATAAATAAAGCA	TTTCTCCGGCAGTT	780	
Db	12220	GAGGGTCGGAGGCTGTG	CAAAATCTAGCTCCATAAATAAAGCA	TTTCTCCGGCAGTT	12279	
QY	781	TCTCAAAAGTAGAAAGGTTA	CATTTAAGGTTCGGTTGTTAGCATTT	CAGTGTTCGCGA	840	
Db	12280	TCTCAAAAGTAGAAAGGTTA	CATTTAAGGTTCGGTTGTTAGCATTT	CAGTGTTCGCGA	12339	
QY	841	CCTCAGCTACAGCATCCCTG	CAAGGCTCGGGAGACCCAGAGTTT	CTCGCCCTTAGAT	900	
Db	12340	CCTCAGCTACAGCATCCCTG	CAAGGCTCGGGAGACCCAGAGTTT	CTCGCCCTTAGAT	12399	
QY	901	CCAAACTTGAGCAACCCGG	AGTCTGGAATTCCTGGGAAGTCC	CTCAGCTGTCGCGTTGT	960	
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QY	961	CCCGGGCCCCAGGCTG	GAGGGGACAGTGGCCGTGTGCG	1001		
Db	12460	CCCGGGCCCCAGGCTG	GAGGGGACAGTGGCCGTGTGCG	12500		

RESULT 3
US-09-994-427A-1
; Sequence 1, Application US/09994427A
; Patent No. US20020128221A1
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Schiff, J. Michael
; TITLE OF INVENTION: GLYCOSYLTRANSFERASE VECTORS FOR TREATING CANCER
; FILE REFERENCE: 083.002
; CURRENT APPLICATION NUMBER: US/09/994,427A
; CURRENT FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: 60/253,395
; PRIOR FILING DATE: 2000-11-27
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1									
; LENGTH: 15418									
; TYPE: DNA									
; ORGANISM: Homo sapiens									
US-09-994-427A-1									
Query Match 100.0%; Score 1001; DB 3; Length 15418;									
Best Local Similarity 100.0%; Pred. No. 1.4e-294;									
Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
Qy	1	GGCTGGGATATACAGGCACCGCCACCATGCGCCAGCTAAATTTTTTTGTATTTTGTAGTAGAGA	60						
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Qy	61	CGGGGTGGGGGTGGGGTTACATGTTGGCGAGGCTGGTCTCGAACTTCTGACCTCAGA	120						
Db	11560	CGGGGTGGGGGTGGGGTTACATGTTGGCGAGGCTGGTCTCGAACTTCTGACCTCAGA	11619						
Qy	121	TGATCCACCTGCTCTGCTCTCTTAAGTGCTGGGATACAGGTGTGAGCCACCATGCCCA	180						
Db	11620	TGATCCACCTGCTCTGCTCTCTTAAGTGCTGGGATACAGGTGTGAGCCACCATGCCCA	11679						
Qy	181	GCTCAGAAATTACTCTGTTTAGAAACATCTGGGTCCTGAGGTAGGAAGCTCACCCCACTCA	240						
Db	11680	GCTCAGAAATTACTCTGTTTAGAAACATCTGGGTCCTGAGGTAGGAAGCTCACCCCACTCA	11739						
Qy	241	AGTGTGTGGTGTGTTTAAGCCAATGATAGAAATTTTTTTTATTTGTTGTAGAACTCTTTGA	300						
Db	11740	AGTGTGTGGTGTGTTTAAGCCAATGATAGAAATTTTTTTTATTTGTTGTAGAACTCTTTGA	11799						
Qy	301	TGTTTTACACTGTGATGACTAAGACATCATCAGCTTTTCAAAGACACACTAACTGCACCC	360						
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Qy	361	ATAAATCTGGGTGTCCTCTGGGTATCAGCGATCTTCAATGAAATCCGGGAGGCGTTTCC	420						
Db	11860	ATAAATCTGGGTGTCCTCTGGGTATCAGCGATCTTCAATGAAATCCGGGAGGCGTTTCC	11919						
Qy	421	TCGCCATGCACATGGTGTTAAATTTACTTCAGCATAAATCTTCTGCTTCCAATTTCTTCTTC	480						
Db	11920	TCGCCATGCACATGGTGTTAAATTTACTTCAGCATAAATCTTCTGCTTCCAATTTCTTCTTC	11979						
Qy	481	CTCTTTTAAATTTGTTTTCTATGTTGGCTTCTCTGCAGAGAACACAGTGTAGCTACA	540						
Db	11980	CTCTTTTAAATTTGTTTTCTATGTTGGCTTCTCTGCAGAGAACACAGTGTAGCTACA	12039						
Qy	541	ACTTAATCTTGTGGAACAAATTTTCCAAACCGCCCTTTGCCCTAGTGCAGAGACAA	600						
Db	12040	ACTTAATCTTGTGGAACAAATTTTCCAAACCGCCCTTTGCCCTAGTGCAGAGACAA	12099						
Qy	601	TTCAAAACACAGCCCTTTAAAAGGCTTAGGGATCACTAAGGGGATTTCTAGAAGAGCG	660						
Db	12100	TTCAAAACACAGCCCTTTAAAAGGCTTAGGGATCACTAAGGGGATTTCTAGAAGAGCG	12159						
Qy	661	ACCGTAATCTTAAGTATTTTACAAGCAGGCTTAACTCTCAGCAGCGCTGACAGCCGAGG	720						
Db	12160	ACCGTAATCTTAAGTATTTTACAAGCAGGCTTAACTCTCAGCAGCGCTGACAGCCGAGG	12219						
Qy	721	GAGGGTCGAGGCGCTGTTCAAATGCTAGCTCCATTAATTAAGCAATTTCTCCGGCAGTT	780						
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Qy	841	CCTCAGCTACAGCATCCTCGAAGGCTCGGAGACCCAGAAGTTTTCGCCCCCTTAGAT	900						
Db	12340	CCTCAGCTACAGCATCCTCGAAGGCTCGGAGACCCAGAAGTTTTCGCCCCCTTAGAT	12399						
Qy	901	CCAAACTTAGGCAACCCGGAGTCTGGAATTCCTGGGAAGTCTCTCAGCTGTCTCGGGTTGT	960						
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Db 12460 GCGGGGCCCCAGTCTGGAGGGACCAAGTGGCGGTGTGGC 12500

RESULT 4
US-09-995-419A-1
; Sequence 1, Application US/09995419A
; Publication No. US20030032187A1
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: McWhir, Jim
; APPLICANT: Gold, Joseph D.
; TITLE OF INVENTION: 096,004 - SeqList
; FILE REFERENCE: 096,004 - SeqList
; CURRENT APPLICATION NUMBER: US/09/995,419A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 60/253,357
; PRIOR FILING DATE: 2000-11-27
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 15418
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-995-419A-1

Query Match 100.0%; Score 1001; DB 3; Length 15418;
Best Local Similarity 100.0%; Pred. No. 1.4e-294;
Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGCCTGGGATTACAGGCACCCGCCACCATGCCAGCTAAATTTTGTATTTTGTAGTAGAGA 60
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Qy 61 CGGGGGTGGGGTGGGGTTCACCATGTGGCCAGCTGGTCTCGAACTTCCTGACCTCAGA 120
Db 11560 CGGGGGTGGGGTGGGGTTCACCATGTGGCCAGCTGGTCTCGAACTTCCTGACCTCAGA 11619

Qy 121 TGATCCACCTGCCTCTGCCTCCTAAAGTGTGGGATTACAGGTGTGAGCCACCATGCCCA 180
Db 11620 TGATCCACCTGCCTCTGCCTCCTAAAGTGTGGGATTACAGGTGTGAGCCACCATGCCCA 11679

Qy 181 GCTCAGAAATTTACTCTGTTTAGAAACATCTGGTCTGAGGTAGGAAGCTCACCCCACTCA 240
Db 11680 GCTCAGAAATTTACTCTGTTTAGAAACATCTGGTCTGAGGTAGGAAGCTCACCCCACTCA 11739

Qy 241 AGTGTGTGTGTTTTTAAGCCATGATAGAAATTTTATTTATTTTGTAGAACACTCTTGA 300
Db 11740 AGTGTGTGTGTTTTTAAGCCATGATAGAAATTTTATTTATTTTGTAGAACACTCTTGA 11799

Qy 301 TGTTTTACATGTGATCACTAAGACATCATCAGCTTTTCAAAGACACACTAACTGCACCC 360
Db 11800 TGTTTTACATGTGATCACTAAGACATCATCAGCTTTTCAAAGACACACTAACTGCACCC 11859

Qy 361 ATAATACCTGGGGTGTCTTCTGGGTATCAGGCATCTTCATTTGAATGCCGGAGGGCTTTCC 420
Db 11860 ATAATACCTGGGGTGTCTTCTGGGTATCAGGCATCTTCATTTGAATGCCGGAGGGCTTTCC 11919

Qy 421 TCGCCATGCACATGGTGTAACTTACTCCAGCATATCTCTGCTTCAATTTCTTCTTTC 480
Db 11920 TCGCCATGCACATGGTGTAACTTACTCCAGCATATCTCTGCTTCAATTTCTTCTTTC 11979

Qy 481 CCTCTTTTAAATTTGTTTCTATGTGGCTTCTCTGCAGAGAACAGGTAGGTACACA 540
Db 11980 CCTCTTTTAAATTTGTTTCTATGTGGCTTCTCTGCAGAGAACAGGTAGGTAGGTACACA 12039

Qy 541 ACTTAACTTTTGTGGAAACAAATTTTCCAAACCGCCCTTTGGCCTAGTGGCAGAGCAA 600
Db 12040 ACTTAACTTTTGTGGAAACAAATTTTCCAAACCGCCCTTTGGCCTAGTGGCAGAGCAA 12099

Qy 601 TTCACAAACACAGCCCTTTTAAAGGCTTAGGATCACTAAGGGGATTTTCTAGAAGAGCG 660
Db 12100 TTCACAAACACAGCCCTTTTAAAGGCTTAGGATCACTAAGGGGATTTTCTAGAAGAGCG 12159

Qy 661 ACCCGTAATCCTTAAGTATTTTACAAGACGAGGCTTAACTCCAGCGAGCGTGACAGCCCAGG 720
Db 12160 ACCCGTAATCCTTAAGTATTTTACAAGACGAGGCTTAACTCCAGCGAGCGTGACAGCCCAGG 12219

Qy 721 GAGGGTGGAGGCTGTGTTCAAAATGCTAGCTCATATAAATAAGCAATTTCTCCGGCAGTT 780
Db 12220 GAGGGTGGAGGCTGTGTTCAAAATGCTAGCTCATATAAATAAGCAATTTCTCCGGCAGTT 12279

Qy 781 TCTGAAAGTAGGAAAGGTTACATTTAAGTGTGGTGTGTAGCATTTCACTGTTTGCCTGA 840
Db 12280 TCTGAAAGTAGGAAAGGTTACATTTAAGTGTGGTGTGTAGCATTTCACTGTTTGCCTGA 12339

Qy 841 CCTCAGCTACAGCATCCCTGCAAGGCTCGGGAGACCCAGAACTTCTCGCCCTTAGAT 900
Db 12340 CCTCAGCTACAGCATCCCTGCAAGGCTCGGGAGACCCAGAACTTCTCGCCCTTAGAT 12399

Qy 901 CCAAACTTGAGCAACCCGAGTCTGGAATCTCGGGAAGTCTCAGCTGTCTCGCGTGT 960
Db 12400 CCAAACTTGAGCAACCCGAGTCTGGAATCTCGGGAAGTCTCAGCTGTCTCGCGTGT 12459

Qy 961 GCGGGGCCCCAGGCTCTGGAGGGGACCATGTCGCGGTGTGGC 1001
Db 12460 GCGGGGCCCCAGGCTCTGGAGGGGACCATGTCGCGGTGTGGC 12500

RESULT 5
US-10-141-220-1
; Sequence 1, Application US/10141220
; Publication No. US20030040111A1
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Gold, Joseph
; APPLICANT: Lebkowski, Jane
; TITLE OF INVENTION: Tpacked stem cells
; FILE REFERENCE: 096/003
; CURRENT APPLICATION NUMBER: US/10/141,220
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: US/09/783,203
; PRIOR FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: 60/253,443
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/253,357
; PRIOR FILING DATE: 2000-11-27
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 15418
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-141-220-1

Query Match 100.0%; Score 1001; DB 5; Length 15418;
Best Local Similarity 100.0%; Pred. No. 1.4e-294;
Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGCCTGGGATTACAGGCACCCGCCACCATGCCAGCTAAATTTTGTATTTTGTAGTAGAGA 60
Db 11500 GGCCTGGGATTACAGGCACCCGCCACCATGCCAGCTAAATTTTGTATTTTGTAGTAGAGA 11559

Qy 61 CGGGGGTGGGGTGGGGTTCACCATGTGGCCAGCTGGTCTCGAACTTCCTGACCTCAGA 120
Db 11560 CGGGGGTGGGGTGGGGTTCACCATGTGGCCAGCTGGTCTCGAACTTCCTGACCTCAGA 11619

Qy 121 TGATCCACCTGCCTCTGCCTCCTAAAGTGTGGGATTACAGGTGTGAGCCACCATGCCCA 180
Db 11620 TGATCCACCTGCCTCTGCCTCCTAAAGTGTGGGATTACAGGTGTGAGCCACCATGCCCA 11679

Qy 181 GCTCAGAAATTTACTCTGTTTAGAAACATCTGGTCTGAGGTAGGAAGCTCACCCCACTCA 240
Db 11680 GCTCAGAAATTTACTCTGTTTAGAAACATCTGGTCTGAGGTAGGAAGCTCACCCCACTCA 11739

Qy 241 AGTGTGTGTGTTTTTAAGCCATGATAGAAATTTTATTTATTTTGTAGAACACTCTTGA 300
Db 11740 AGTGTGTGTGTTTTTAAGCCATGATAGAAATTTTATTTATTTTGTAGAACACTCTTGA 11799

Qy 301 TGTTTTACATGTGATCACTAAGACATCATCAGCTTTTCAAAGACACACTAACTGCACCC 360
Db 11800 TGTTTTACATGTGATCACTAAGACATCATCAGCTTTTCAAAGACACACTAACTGCACCC 11859

Qy 361 ATAATACCTGGGGTGTCTTCTGGGTATCAGGCATCTTCATTTGAATGCCGGAGGGCTTTCC 420
Db 11860 ATAATACCTGGGGTGTCTTCTGGGTATCAGGCATCTTCATTTGAATGCCGGAGGGCTTTCC 11919

Qy 421 TCGCCATGCACATGGTGTAACTTACTCCAGCATATCTCTGCTTCAATTTCTTCTTTC 480
Db 11920 TCGCCATGCACATGGTGTAACTTACTCCAGCATATCTCTGCTTCAATTTCTTCTTTC 11979

Qy 481 CCTCTTTTAAATTTGTTTCTATGTGGCTTCTCTGCAGAGAACAGGTAGGTAGGTACACA 540
Db 11980 CCTCTTTTAAATTTGTTTCTATGTGGCTTCTCTGCAGAGAACAGGTAGGTAGGTAGGTACACA 12039

Qy 541 ACTTAACTTTTGTGGAAACAAATTTTCCAAACCGCCCTTTGGCCTAGTGGCAGAGCAA 600
Db 12040 ACTTAACTTTTGTGGAAACAAATTTTCCAAACCGCCCTTTGGCCTAGTGGCAGAGCAA 12099
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Db 12460 GCCGGGGCCCCAGGCTCTGGAGGGGACCAAGTGGCGGTGGC 12500
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Db 12460 TTCAAAACACACAGCCCTTTTAAAAAGGCTTAGGATCACTAAGGGGATTTCTAGAGAGCG 12159
Qy 661 ACCGTAATCTTAAGTATTTTACAAGACGAGGCTAAACCTCAGCGAGCGTGACACCCAGG 720
|||||
Db 12160 ACCGTAATCTTAAGTATTTTACAAGACGAGGCTAAACCTCAGCGAGCGTGACACCCAGG 12219
|||||
Qy 721 GAGGTCGCGAGGCTCTTCAAAATGCTAGCTCCATTAATAAAGCAATTTCTCCGGCAGTT 780
|||||
Db 12220 GAGGTCGCGAGGCTCTTCAAAATGCTAGCTCCATTAATAAAGCAATTTCTCCGGCAGTT 12279
|||||
Qy 781 TCTGAAAGTAGGAAAGGTTACATTTTAAGGTTGGGTTTGTAGCATTTTCAGTGTGTGCGCA 840
|||||
Db 12280 TCTGAAAGTAGGAAAGGTTACATTTTAAGGTTGGGTTTGTAGCATTTTCAGTGTGTGCGCA 12339
|||||
Qy 841 CCTCAGCTACAGCATCTCTGCAAGGCTCTGGGAGACCCAGAGTTTCTCGCCCTTAGAT 900
|||||
Db 12340 CCTCAGCTACAGCATCTCTGCAAGGCTCTGGGAGACCCAGAGTTTCTCGCCCTTAGAT 12399
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Qy 901 CCAAACTTGAGCAACCGGAGTCTGGATTCTCGGAGTCTCAGCTGTCTCGGGTTGT 960
|||||
Db 12400 CCAAACTTGAGCAACCGGAGTCTGGATTCTCGGAGTCTCAGCTGTCTCGGGTTGT 12459
|||||
Qy 961 GCCGGGGCCCCAGGCTCTGGAGGGGACCAAGTGGCGGTGGC 1001
|||||
Db 12460 GCCGGGGCCCCAGGCTCTGGAGGGGACCAAGTGGCGGTGGC 12500
|||||

RESULT 8
US-10-674-836-1
; Sequence 1, Application US/10674836
; Publication No. US20040072787A1
; GENERAL INFORMATION:
; APPLICANT: Morin, Gregg B.
; APPLICANT: Lichtesteiner, Serge
; APPLICANT: Vasserot, Alain
; APPLICANT: Adams, Robert R.
; APPLICANT: Geron Corporation
; TITLE OF INVENTION: Telomerase Reverse Transcriptase Transcriptional
; FILE REFERENCE: 019/246P
; CURRENT APPLICATION NUMBER: US/10/674,836
; PRIOR FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: US/09/244,438
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 15418
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Human TERT promoter
US-10-674-836-1

Query Match 100.0%; Score 1001; DB 7; Length 15418;
Best Local Similarity 100.0%; Pred. No. 1.4e-294; Indels 0; Gaps 0;
Matches 1001; Conservative 0; Mismatches 0;

Qy 1 GGCTGGGATTACAGGACCCGCCACCATGCGCAGCTAAATTTTGTATTTTAGTAGAGA 60
Db 11500 GGCTGGGATTACAGGACCCGCCACCATGCGCAGCTAAATTTTGTATTTTAGTAGAGA 11559
Qy 61 CGGGGGTGGGGTGTACCATGTTGGCCAGGCTGCTCGAACTTCTGACCTCAGA 120
Db 11560 CGGGGGTGGGGTGTACCATGTTGGCCAGGCTGCTCGAACTTCTGACCTCAGA 11619
Qy 121 TGATCCACCTGCTCTGCCCTCTAAAGTCTGGGATTACAGGTGTGAGCCACCATGCCCA 180
Db 11620 TGATCCACCTGCTCTGCCCTCTAAAGTCTGGGATTACAGGTGTGAGCCACCATGCCCA 11679
Qy 181 GCTCAGAAATTACTCTGTTTGTAGAAACATCTGGGTCTGAGGTAGGAAGCTCACCCCACTCA 240
Db 11680 GCTCAGAAATTACTCTGTTTGTAGAAACATCTGGGTCTGAGGTAGGAAGCTCACCCCACTCA 11739
Qy 241 AGTGTGTGTGTTTAAAGCAATGATAGAAATTTTATTTTGTAGAACACTCTTGA 300
Db 11740 AGTGTGTGTGTTTAAAGCAATGATAGAAATTTTATTTTGTAGAACACTCTTGA 11799
Qy 301 TGTTTTACCTGTGATGACCTAAGACATCATCAGCTTTTCAAAGACACACTAACTGCACCC 360
Db 11800 TGTTTTACCTGTGATGACCTAAGACATCATCAGCTTTTCAAAGACACACTAACTGCACCC 11859
Qy 361 ATAATACCTGGGTGCTCTTGGGTATCAGCATCTTCAATTAATGAAATGCGGGAGGGTTTC 420
Db 11860 ATAATACCTGGGTGCTCTTGGGTATCAGCATCTTCAATTAATGAAATGCGGGAGGGTTTC 11919
Qy 421 TCGCCATGCATGCTGTTAAATTAATCTCCAGCATATCTTCTGCTTCCATTTCTTCTTC 480
Db 11920 TCGCCATGCATGCTGTTAAATTAATCTCCAGCATATCTTCTGCTTCCATTTCTTCTTC 11979
Qy 481 CCTCTTTTAAATTTGTGTTTTCTATGTTGGCTTCTCTGCAGAGAACCAAGTGTAGCTACA 540
Db 11980 CCTCTTTTAAATTTGTGTTTTCTATGTTGGCTTCTCTGCAGAGAACCAAGTGTAGCTACA 12039
Qy 541 ACTTAATCTTTTGTGGAAACAAATTTTCAAACCGCCCTTTGCCCTAGTGTGAGAGACAA 600
Db 12040 ACTTAATCTTTTGTGGAAACAAATTTTCAAACCGCCCTTTGCCCTAGTGTGAGAGACAA 12099
Qy 601 TTCAAAACACAGCCCTTTTAAAAAGGCTTAGGGATCACTAAGGGGATTTCTAGAGAGCG 660
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Qy	241	AGTGTGTGGTGTGTTTAAAGCCAAATGATAGAAATTTTTTATTGTTAGAAACACTCTTGA	300
Db	11740	AGTGTGTGGTGTGTTTAAAGCCAAATGATAGAAATTTTTTATTGTTAGAAACACTCTTGA	11799
Qy	301	TGTTTTACACTGTGATGACTAAGACATCATCAGCTTTTCAAGACACACTAATGACACC	360
Db	11800	TGTTTTACACTGTGATGACTAAGACATCATCAGCTTTTCAAGACACACTAATGACACC	11859
Qy	361	ATAATACTGGGGTGCTTCTGGGTATCAGCGATCTTCATTGAATCGCGAGGCGTTTCC	420
Db	11860	ATAATACTGGGGTGCTTCTGGGTATCAGCGATCTTCATTGAATCGCGAGGCGTTTCC	11919
Qy	421	TCGCCATGCACATGGTGTTAAATTACTCCAGCAATAATCTTCTGCTTCCATTTTCTCTCTC	480
Db	11920	TCGCCATGCACATGGTGTTAAATTACTCCAGCAATAATCTTCTGCTTCCATTTTCTCTCTC	11979
Qy	481	CTCTTTTAAAAATGTGTTTTCTATGTGGTCTCTGCGAGAAACCAAGTGTAAAGCTACA	540
Db	11980	CTCTTTTAAAAATGTGTTTTCTATGTGGTCTCTGCGAGAAACCAAGTGTAAAGCTACA	12039
Qy	541	ACTTAACCTTTGTGGAAACAAATTTTCCAAA CGGCCCTTTGCCCCTAGTGGCAGAGACAA	600
Db	12040	ACTTAACCTTTGTGGAAACAAATTTTCCAAA CGGCCCTTTGCCCCTAGTGGCAGAGACAA	12099
Qy	601	TTCAACAACACAGCCCTTTTAAAAAGGCTTAGGGATCACTAAGGGGANTTCTAGAGAGCG	660
Db	12100	TTCAACAACACAGCCCTTTTAAAAAGGCTTAGGGANCACTAAGGGGANTTCTAGAGAGCG	12159
Qy	661	ACCCGTAATCCTTAAGTATTTTACAAGACGAGGCTAACTCCAGCGAGCGTGA CAGCCCAGG	720
Db	12160	ACCCGTAATCCTTAAGTATTTTACAAGACGAGGCTAACTCCAGCGAGCGTGA CAGCCCAGG	12219
Qy	721	GAGGGTCGAGGCGCTGTTCAAATGCTAGCTCCATAAATAAAGCAATTTCTCCGGCAGTT	780
Db	12220	GAGGGTCGAGGCGCTGTTCAAATGCTAGCTCCATAAATAAAGCAATTTCTCCGGCAGTT	12279
Qy	781	TCTGAAAGTAGGAAGGTACATTTAAGTTGCGTTGTAGCATTTAGTGTGTTGCCGA	840
Db	12280	TCTGAAAGTAGGAAGGTACATTTAAGTTGCGTTGTAGCATTTAGTGTGTTGCCGA	12339
Qy	841	CCTCAGCTACAGCATCCCTCAAGGCGCTGGGAGACCAGAAGTTTCTCGCCCCCTTAGAT	900
Db	12340	CCTCAGCTACAGCATCCCTCAAGGCGCTGGGAGACCAGAAGTTTCTCGCCCCCTTAGAT	12399
Qy	901	CCAAACTTGAGCAACCGGAGTCTGGAATCTCTGGGAAGTCTCAGCTGTCCTCGCGTTGT	960
Db	12400	CCAAACTTGAGCAACCGGAGTCTGGAATCTCTGGGAAGTCTCAGCTGTCCTCGCGTTGT	12459
Qy	961	CGCGGGGCCCCAGGCTGTGGAGGGGACCAAGTGGCCGTGTGCG	1001
Db	12460	CGCGGGGCCCCAGGCTGTGGAGGGGACCAAGTGGCCGTGTGCG	12500

RESULT 9

US-10-811-012-1
; Sequence 1, Application US/10811012
; Publication No. US20040152189A1
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: McWhir, Jim
; APPLICANT: Gold, Joseph D.
; APPLICANT: Schiff, J. Michael
; TITLE OP INVENTION: Selective Antibody Targeting of Undifferentiated Stem Cells
; FILE REFERENCE: 036, 006D- SeqList
; CURRENT APPLICATION NUMBER: US/10/811,012
; CURRENT FILING DATE: 2004-03-26
; PRIOR APPLICATION NUMBER: 05/995,419
; PRIOR FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 60/253,357
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/253,443
; PRIOR FILING DATE: 2000-11-27

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; PRIOR APPLICATION NUMBER: 60/253,395
; PRIOR FILING DATE: 2000-11-27
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 15418
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-811-012-1

Query Match          100.0%; Score 1001; DB 7; Length 15418;
Best Local Similarity 100.0%; Pred. No. 1.4e-294;
Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCGTGGGATTA CAGGCACCCGCCACCATGCCAGCTAAATTTTTGTGATTTTAGTAGAGA 60
Db 11500 GGCTGGGATTA CAGGCACCCGCCACCATGCCAGCTAAATTTTTGTGATTTTAGTAGAGA 11559

Qy 61 CGGGGGTGGGGGTGGGGTTTACCATTGTTGGCCAGGCTGGTCTCGAACTTCTGACCTCAGA 120
Db 11560 CGGGGGTGGGGGTGGGGTTTACCATTGTTGGCCAGGCTGGTCTCGAACTTCTGACCTCAGA 11619

Qy 121 TGATCCACCTCGCTCTGCTCTCTAAAGTGTCTGGGATTTACAGGTGTGAGCCACCATGCCCA 180
Db 11620 TGATCCACCTCGCTCTGCTCTCTAAAGTGTCTGGGATTTACAGGTGTGAGCCACCATGCCCA 11679

Qy 181 GCTCAGAAATTTACTCTGTTTAAAGAA CATCTGGGTCTGAGGTAGGAAGCTCACCCCACTCA 240
Db 11680 GCTCAGAAATTTACTCTGTTTAAAGAA CATCTGGGTCTGAGGTAGGAAGCTCACCCCACTCA 11739

Qy 241 AGTGTGTGGTGTGTTTAAAGCCAAATGATAGAAATTTTTTTATGTTGTAGAACACTCTTGA 300
Db 11740 AGTGTGTGGTGTGTTTAAAGCCAAATGATAGAAATTTTTTTATGTTGTAGAACACTCTTGA 11799

Qy 301 TGTTTTACATGTGATGACTAAGACATCATCAGCTTTTCAAAGACACACTAACTGCACCC 360
Db 11800 TGTTTTACATGTGATGACTAAGACATCATCAGCTTTTCAAAGACACACTAACTGCACCC 11859

Qy 361 ATAATACCTGGGGTGTCTTCTGGGTATCAGCGATCTTCATTGAATGCCGGAGCGTTTCC 420
Db 11860 ATAATACCTGGGGTGTCTTCTGGGTATCAGCGATCTTCATTGAATGCCGGAGCGTTTCC 11919

Qy 421 TCGGCATGCACATGGTGTGTTAATCTCCAGCATAAATCTTCTGCTTCGATTTCTTCTTTC 480
Db 11920 TCGGCATGCACATGGTGTGTTAATCTCCAGCATAAATCTTCTGCTTCGATTTCTTCTTTC 11979

Qy 481 CCTCTTTTAAATATGCTGTTTTCTATGTTGGCTTCTCTGCAGAGAACACAGTGAAGCTACA 540
Db 11980 CCTCTTTTAAATATGCTGTTTTCTATGTTGGCTTCTCTGCAGAGAACACAGTGAAGCTACA 12039

Qy 541 ACTTAACTTTTGTGGAAACAAATTTTCCAAACCGCCCTTTGCTTCCCTAGTGGCAGAGACAA 600
Db 12040 ACTTAACTTTTGTGGAAACAAATTTTCCAAACCGCCCTTTGCTTCCCTAGTGGCAGAGACAA 12099

Qy 601 TTCAAAACACACAGCCCTTTAAAGGCTTAGGGATCACTAAGGGGATTTCTAGAAGAGCG 660
Db 12100 TTCAAAACACACAGCCCTTTAAAGGCTTAGGGATCACTAAGGGGATTTCTAGAAGAGCG 12159

Qy 661 ACCGGTATCTCTAGTATTTACAAGCAGGCGTTAACTCCAGCGAGCGTGACACGCCCAGG 720
Db 12160 ACCGGTATCTCTAGTATTTACAAGCAGGCGTTAACTCCAGCGAGCGTGACACGCCCAGG 12219

Qy 721 GAGGGTGGAGGCCCTGTTCAAAATGCTAGCTCCATAATAAGCAATTTCTCCGGCAGATT 780
Db 12220 GAGGGTGGAGGCCCTGTTCAAAATGCTAGCTCCATAATAAGCAATTTCTCCGGCAGATT 12279

Qy 781 TCTGAAGTAGGAAAGGTTACATTTAAGTGTGCTTTGTAGCAATTTCACTGTTTGC CGA 840
Db 12280 TCTGAAGTAGGAAAGGTTACATTTAAGTGTGCTTTGTAGCAATTTCACTGTTTGC CGA 12339

Qy 841 CCTCAGCTACAGCATCCCTGCAAGGCTCGGGAGACCCAGAGTTTCTCGCCCTTAGAT 900
Db 12340 CCTCAGCTACAGCATCCCTGCAAGGCTCGGGAGACCCAGAGTTTCTCGCCCTTAGAT 12399

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Qy 901 CCAAACTTGAGCAACCCGGAGTCTGGATTCTGGGAAGTCTCAGCTGTCTCGCGTTGT 960
Db 12400 CCAAACTTGAGCAACCCGGAGTCTGGATTCTGGGAAGTCTCAGCTGTCTCGCGTTGT 12459
Qy 961 GCCGGGGCCCCAGGTCTGGAGGGGACCAAGTGGCCGTGTGGC 1001
Db 12460 GCCGGGGCCCCAGGTCTGGAGGGGACCAAGTGGCCGTGTGGC 12500

RESULT 10

US-10-456-830-1
; Sequence 1, Application US/10456830
; Publication No. US20040248246A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as
; APPLICANT: represented by the Secretary of the Department of Health and
; APPLICANT: Human Services
; APPLICANT: Horikawa, Izumi
; APPLICANT: Barrett, J. Carl
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ENHANCING DIFFERENTIAL EXPRESSION
; FILE REFERENCE: 4239-63008
; CURRENT APPLICATION NUMBER: US/10/456,830
; CURRENT FILING DATE: 2003-06-05
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 4293
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (345)..(3609)
; OTHER INFORMATION: Region identical to HBV integration site in huH-4 cell line
; FEATURE:
; NAME/KEY: protein bind
; LOCATION: (3729)..(3734)
; OTHER INFORMATION: Upstream E-box
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3916)..(3916)
; OTHER INFORMATION: Major transcription initiation site
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (3916)..(3970)
; OTHER INFORMATION: 5' untranslated region of mRNA
; FEATURE:
; NAME/KEY: protein bind
; LOCATION: (3937)..(3942)
; OTHER INFORMATION: Downstream E-box
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3971)..(4189)
; OTHER INFORMATION: Exon 1
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: (4029)..(4050)
; OTHER INFORMATION: GM2 primer binding site
; FEATURE:
; NAME/KEY: Intron
; LOCATION: (4190)..(4293)
; OTHER INFORMATION: Intron 1
US-10-456-830-1

Query Match 98.8%; Score 988.6; DB 8; Length 4293;
Best Local Similarity 99.8%; Pred. No. 4.3e-291;
Matches 999; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
Qy 1 GGCTGGGATTACAGGACCCGCCACCATGCCAGCTAATTTTGTATTTTGTAGTAGAGA 60
Db 1927 GGCTGGGATTACAGGACCCGCCACCATGCCAGCTAATTTTGTATTTTGTAGTAGAGA 1986
Qy 61 CGGGGGTGGGGGTTCACCATGTGGCCAGGCTGGTCTCGAACTTCTGACCTCAGA 120

Db 1987 CGGGGGTGGGGGTGGGGTTTCCAAATGTTGGCCAGGCTGGTCTCGAACTTCTGACCTCAGA 2046
Qy 121 TGATCCACCTGCTCTGCTCCCTAAAGTGTCTGGGATTCACAGGTGTGAGGCCACCATGCCCA 180
Db 2047 TGATCCACCTGCTCTGCTCCCTAAAGTGTCTGGGATTCACAGGTGTGAGGCCACCATGCCCA 2106
Qy 181 GCTCAGAAATTTACTCTGTTTAAAGCAATCTGGGTCTGAGGTAGGAAGCTACCCCACTCA 240
Db 2107 GCTCAGAAATTTACTCTGTTT - GAAACATCTGGGTCTGAGGTAGGAAGCTACCCCACTCA 2165
Qy 241 AGTGTCTGCTGTTTAAAGCAATTCAGTAAATTTTATTTTATTTTGTAGTAACTCTTGA 300
Db 2166 AGTGTCTGCTGTTTAAAGCAATTCAGTAAATTTTATTTTATTTTGTAGTAACTCTTGA 2225
Qy 301 TGTPTTACACTGTGATGACTTAAGACATCATCAGCTTTTCAAAGACACACTAACTGCACCC 360
Db 2226 TGTPTTACACTGTGATGACTTAAGACATCATCAGCTTTTCAAAGACACACTAACTGCACCC 2285
Qy 361 ATAATCTGGGGTGTCTTCTGGGTATCAGGATCTTCAATGATCCGGGAGGGGTTTCC 420
Db 2286 ATAATCTGGGGTGTCTTCTGGGTATCAGGATCTTCAATGATCCGGGAGGGGTTTCC 2345
Qy 421 TCGCCATGCACATGCTGTTAAATTTACTCCAGCATAATCTTCTGCTTCCATTTCTTCTTTC 480
Db 2346 TCGCCATGCACATGCTGTTAAATTTACTCCAGCATAATCTTCTGCTTCCATTTCTTCTTTC 2405
Qy 481 CCTCTTTTAAATTTGTGTTTCTATGTTGGCTTCTCTGCAGAGAACACAGTGTAGCTACA 540
Db 2406 CCTCTTTTAAATTTGTGTTTCTATGTTGGCTTCTCTGCAGAGAACACAGTGTAGCTACA 2465
Qy 541 ACTTAATCTTTGTTGGAAACAAATTTTCCAAACCGCCCTTTGCCCTAGTGGCAGAGACAA 600
Db 2466 ACTTAATCTTTGTTGGAAACAAATTTTCCAAACCGCCCTTTGCCCTAGTGGCAGAGACAA 2525
Qy 601 TTCACAAACACAGCCCTTTTAAAGGCTTAGGGATCACTAAGGGGATTTCTAGAAAGAGCG 660
Db 2526 TTCACAAACACAGCCCTTTTAAAGGCTTAGGGATCACTAAGGGGATTTCTAGAAAGAGCG 2585
Qy 661 ACCCGTAATCCTAAGTATTTTACAAGACAGGCTTAACCTCCAGCGAGCGTGACAGCCCAGG 720
Db 2586 ACCVGTAATCCTAAGTATTTTACAAGACAGGCTTAACCTCCAGCGAGCGTGACAGCCCAGG 2645
Qy 721 GAGGGTGCAGGCGCTGTTCAATGCTAGCTCCATAAATAAGCAATTTCTCCGGCAGTT 780
Db 2646 GAGGGTGCAGGCGCTGTTCAATGCTAGCTCCATAAATAAGCAATTTCTCCGGCAGTT 2705
Qy 781 TCTGAAAGTAGGAAAGGTTACATTTTAAGGTTGCGTTTGTAGCATTTTCAAGTGTTCGCGA 840
Db 2706 TCTGAAAGTAGGAAAGGTTACATTTTAAGGTTGCGTTTGTAGCATTTTCAAGTGTTCGCGA 2765
Qy 841 CCTCAGCTACAGCATCCCTGCAAGGCTCGGGAGACCCAGAAGTTTCTCGCCCTTAGAT 900
Db 2766 CCTCAGCTACAGCATCCCTGCAAGGCTCGGGAGACCCAGAAGTTTCTCGCCCTTAGAT 2825
Qy 901 CCAAACTTGAGCAACCCGGAGTCTGGATTCTGGGAAGTCTCAGCTGTCTCGCGTTGT 960
Db 2826 CCAAACTTGAGCAACCCGGAGTCTGGATTCTGGGAAGTCTCAGCTGTCTCGCGTTGT 2885
Qy 961 GCCGGGGCCCCAGGTCTGGAGGGGACCAAGTGGCCGTGTGGC 1001
Db 2886 GCCGGGGCCCCAGGTCTGGAGGGGACCAAGTGGCCGTGTGGC 2926

RESULT 11

US-10-840-455-1
; Sequence 1, Application US/10840455
; Publication No. US20050032094A1
; GENERAL INFORMATION:
; APPLICANT: Bayer Aktiengesellschaft
; APPLICANT: Hagen, Gustav
; APPLICANT: Wick, Maresa
; APPLICANT: Zubov, Dmitry

;; TITLE OF INVENTION: Regulatory DNA Sequences of the Gene for the Human Catalytic
;; TITLE OF INVENTION: Telomerase Subunit, and Their Diagnostic and Therapeutic Use

;; FILE REFERENCE: Lea 32 805C1

;; CURRENT APPLICATION NUMBER: US/10/840,455

;; CURRENT FILING DATE: 2004-05-06

;; PRIOR APPLICATION NUMBER: PCT/EP98/08216

;; PRIOR FILING DATE: 1998-12-22

;; PRIOR APPLICATION NUMBER: US 09/582,246

;; PRIOR FILING DATE: 2000-09-21

;; PRIOR APPLICATION NUMBER: DE19757984.1

;; PRIOR FILING DATE: 1997-12-24

;; NUMBER OF SEQ ID NOS: 44

;; SOFTWARE: PatentIn version 3.2

;; SEQ ID NO 1

;; LENGTH: 5126

;; TYPE: DNA

;; ORGANISM: Homo sapiens

;; US-10-840-455-1

Query Match 97.2%; Score 972.8; DB 8; Length 5126;

Best Local Similarity 99.5%; Pred. No. 3.3e-286;

Matches 997; Conservative 0; Mismatches 2; Indels 3; Gaps 2;

Qy 1 GGCTGGGATTACAGGACCCGCCACCATGCCAGCTAATTTTGTATTTTAGTAGAGA 60

Db 3080 GGCTGGGATTACAGGACCCGCCACCATGCCAGCTAATTTTGTATTTTAGTAGAGA 3139

Qy 61 CGGGGGTGGGGTGGGGTCCACCATGTTGGCCAGCTGCTCGAATCTCGACTCAGA 120

Db 3140 CGGGGGT--GGGTGGGGTTCACCATGTTGGCCAGCTGCTCGAATCTCGACTCAGA 3197

Qy 121 TGATCCACCTGCCTCTGCCTCTTAAGTCTGGGATTACAGGTGAGCCACCATGCCCA 180

Db 3198 TGATCCACCTGCCTCTGCCTCTTAAGTCTGGGATTACAGGTGAGCCACCATGCCCA 3257

Qy 181 GCTCAGAAATTTACTCTGTTTAAACATCTGGGTCTGAGGTAGGAAGCTACCCACTCA 240

Db 3258 GCTCAGAAATTTACTCTGTTTAAACATCTGGGTCTGAGGTAGGAAGCTACCCACTCA 3317

Qy 241 AGTGTGTGGTGTTTTAAAGCAATGATAGAAATTTTATTTTGTAGTAACTCTTGA 300

Db 3318 AGTGTGTGGTGTTTTAAAGCAATGATAGAAATTTTATTTTGTAGTAACTCTTGA 3377

Qy 301 TGTTTTACATGTGATGACTAAGACATCATCAGCTTTTCAAAGACACACTAATGACCC 360

Db 3378 TGTTTTACATGTGATGACTAAGACATCATCAGCTTTTCAAAGACACACTAATGACCC 3437

Qy 361 ATAATACCTGGGTGTCTTCTGGGTATCAGCATCTTCAATGAAATGCCGGAGGGTTC 420

Db 3438 ATAATACCTGGGTGTCTTCTGGGTATCAGCATCTTCAATGAAATGCCGGAGGGTTC 3497

Qy 421 TCGCCATGCATGTGTGTTTACTCTCAGCATATCTCTGCTCCATTTCTTCTCTTC 480

Db 3498 TCGCCATGCATGTGTGTTTACTCTCAGCATATCTCTGCTCCATTTCTTCTCTTC 3557

Qy 481 CCTCTTTTAAATTTCTGTTTCTATGTTGGCTTCTCTGAGAGAACCTAGTGAAGCTACA 540

Db 3558 CCTCTTTTAAATTTCTGTTTCTATGTTGGCTTCTCTGAGAGAACCTAGTGAAGCTACA 3617

Qy 541 ACTTAACCTTTTGTGGAAACAAATTTTCAAACCGCCCTTTGCCCTAGTGGCAGAGCAA 600

Db 3618 ACTTAACCTTTTGTGGAAACAAATTTTCAAACCGCCCTTTGCCCTAGTGGCAGAGCAA 3677

Qy 601 TTCACAAACAGACCCCTTTAAAGGCTTAGGGATCACTAAGGGGATTTCTAGAGAGCG 660

Db 3678 TTCACAAACAGACCCCTTTAAAGGCTTAGGGATCACTAAGGGGATTTCTAGAGAGCG 3737

Qy 661 ACCCGTAACTTAAGTATTTTAAAGCGAGGCTTAACCTCCAGCGAGCTGACAGCCGAGG 720

Db 3738 ACCCGTAACTTAAGTATTTTAAAGCGAGGCTTAACCTCCAGCGAGCTGACAGCCGAGG 3797

Qy 721 GAGGCTGGGAGGCTGTTTCAATGCTAGCTCCATAATAAGCAATTTCTCCGCGAGTT 780

Db 3798 GAGGCTGGGAGGCTGTTCAAAATGCTAGCTCCATAAATAAAGCAATTTCTCCGCGAGTT 3857

Qy 781 TCTGAAAGTAGGAAAGGTATACATTTAAAGGTTGCGTTTGTAGCAATTTTCAGTGTTCGCGA 840

Db 3858 TCTGAAAGTAGGAAAGGTATACATTTAAAGGTTGCGTTTGTAGCAATTTTCAGTGTTCGCGA 3917

Qy 841 CCTCAGCTACAGCATCTCTGCAAGGCTCGGAGACCCAGAAAGTTTCTCG--CCCTTAGA 899

Db 3918 CCTCAGCTACAGCATCTCTGCAAGGCTCGGAGACCCAGAAAGTTTCTCGCCCTTAGA 3977

Qy 900 TCCAAATCTTGAGCAACCGGGAGTCTGGATTCCTCGGAAGTCTCAGCTGTCTTCGCGTTG 959

Db 3978 TCCAAATCTTGAGCAACCGGGAGTCTGGATTCCTCGGAAGTCTCAGCTGTCTTCGCGTTG 4037

Qy 960 TGCCGGGGCCCCCAGGCTCTGGAGGGGACCAAGTGGCCGCTGTGGC 1001

Db 4038 TGCCGGGGCCCCCAGGCTCTGGAGGGGACCAAGTGGCCGCTGTGGC 4079

RESULT 12

US-10-840-455-3

;; Sequence 3, Application US/10840455

;; Publication No. US20050032094A1

;; GENERAL INFORMATION:

;; APPLICANT: Bayer Aktiengesellschaft

;; APPLICANT: Hagen, Gustav

;; APPLICANT: Wick, Maresa

;; APPLICANT: Zubov, Dmitry

;; TITLE OF INVENTION: Regulatory DNA Sequences of the Gene for the Human Catalytic

;; TITLE OF INVENTION: Telomerase Subunit, and Their Diagnostic and Therapeutic Use

;; FILE REFERENCE: Lea 32 805C1

;; CURRENT APPLICATION NUMBER: US/10/840,455

;; CURRENT FILING DATE: 2004-05-06

;; PRIOR APPLICATION NUMBER: PCT/EP98/08216

;; PRIOR FILING DATE: 1998-12-22

;; PRIOR APPLICATION NUMBER: US 09/582,246

;; PRIOR FILING DATE: 2000-09-21

;; PRIOR APPLICATION NUMBER: DE19757984.1

;; PRIOR FILING DATE: 1997-12-24

;; NUMBER OF SEQ ID NOS: 44

;; SOFTWARE: PatentIn version 3.2

;; SEQ ID NO 3

;; LENGTH: 11276

;; TYPE: DNA

;; ORGANISM: Homo sapiens

;; US-10-840-455-3

Query Match 97.2%; Score 972.8; DB 8; Length 11276;

Best Local Similarity 99.5%; Pred. No. 5e-286;

Matches 997; Conservative 0; Mismatches 2; Indels 3; Gaps 2;

Qy 1 GGCTGGGATTACAGGACCCGCCACCATGCCAGCTAATTTTGTATTTTAGTAGAGA 60

Db 9230 GGCTGGGATTACAGGACCCGCCACCATGCCAGCTAATTTTGTATTTTAGTAGAGA 9289

Qy 61 CGGGGGTGGGGTGGGGTTCACCATGTTGGCCAGGCTGCTCGAACTTCTGACCTCAGA 120

Db 9290 CGGGGGT--GGGTGGGGTTCACCATGTTGGCCAGGCTGCTCGAACTTCTGACCTCAGA 9347

Qy 121 TGATCCACCTGCCTCTGCCTCTTAAGTCTGGGATTTACAGGTGAGCCACCATGCCCA 180

Db 9348 TGATCCACCTGCCTCTGCCTCTTAAGTCTGGGATTTACAGGTGAGCCACCATGCCCA 9407

Qy 181 GCTCAGAAATTTACTCTGTTTAAAGCAATGATAGAAATTTTATTTTGTAGTAACTCTTGA 300

Db 9408 GCTCAGAAATTTACTCTGTTTAAAGCAATGATAGAAATTTTATTTTGTAGTAACTCTTGA 9527

Qy 301 TGTTTTACATGTGATGACTAAGACATCATCAGCTTTTCAAAGACACACTAATGACCC 360

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Db 9528 TGTGTTTACACTGTGATGACTAAGACATCATCAGCTTTTCAAAGACACACTAACTGCACCC 9587

Qy 361 ATATATCTGGGGTCTCTCTGGGTATCAGCGATCTTCATTTGAATGCCGGAGGGGTTTCC 420

Db 9588 ATATATCTGGGGTCTCTCTGGGTATCAGCAATCTTCATTTGAATGCCGGAGGGGTTTCC 9647

Qy 421 TCGCCATGCACATGCTGTTAATTAATCTCAGCATATCTTCGCTTCCATTTCTCTCTTC 480

Db 9648 TCGCCATGCACATGCTGTTAATTAATCTCAGCATATCTTCGCTTCCATTTCTCTCTTC 9707

Qy 481 CCTCTTTTAAATTTGTGTTTCTATGTTGGCTTCTCTCGAGAGAACAGTGTAGCTACA 540

Db 9708 CCTCTTTTAAATTTGTGTTTCTATGTTGGCTTCTCTCGAGAGAACAGTGTAGCTACA 9767

Qy 541 ACTTAACCTTTGTTGGAAACAAATTTTCAAACCCGCCCTTTGCCCTTAGTGCGAGACAA 600

Db 9768 ACTTAACCTTTGTTGGAAACAAATTTTCAAACCCGCCCTTTGCCCTTAGTGCGAGACAA 9827

Qy 601 TTCACAAACACAGCCCTTTTAAAGAGCTTAGGGATCACTAAGGGGATTTCTAGAAAGCG 660

Db 9828 TTCACAAACACAGCCCTTTTAAAGAGCTTAGGGATCACTAAGGGGATTTCTAGAAAGCG 9887

Qy 661 ACCCGTAATCTTAAGTATTTTACAAGACGAGCTTAACCTTCCAGCGAGGCTGACACCCAGG 720

Db 9888 ACCGTAACTCTTAAGTATTTTACAAGACGAGCTTAACCTTCCAGCGAGGCTGACACCCAGG 9947

Qy 721 GAGGGTCGAGGCTGTTCAAATGCTAGCTTCCATTAATTAAGCAATTTCTCCGGCAGTT 780

Db 9948 GAGGGTCGAGGCTGTTCAAATGCTAGCTTCCATTAATTAAGCAATTTCTCCGGCAGTT 10007

Qy 781 TCTCAAAAGTAGGAAGGTTACATTTAAGTTGCGTTGTTAGCAATTTCAAGTTTTCGCGA 840

Db 10008 TCTCAAAAGTAGGAAGGTTACATTTAAGTTGCGTTGTTAGCAATTTCAAGTTTTCGCGA 10067

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Db 10068 CCTCAGCTACAGCATCCTTGAAGGCTTCCGGAGACCCAGAGTTTCTCG-CCCTTTAGA 959

Qy 900 TCGAACTTGAGCAACCCGGAGTCTGATTTCTGGGAAGTCTCCTCAGCTGCTCGGGTTG 959

Db 10128 TCGAACTTGAGCAACCCGGAGTCTGATTTCTGGGAAGTCTCCTCAGCTGCTCGGGTTG 10187

Qy 960 TCGCGGGCCCCAGGCTCTGGAGGGGACCACTGGCCGCTGTGGC 1001

Db 10188 TCGCGGGCCCCAGGCTCTGGAGGGGACCACTGGCCGCTGTGGC 10229

RESULT 13

US-10-840-455-43

Sequence 43, Application US/10840455

Publication No. US20050032094A1

GENERAL INFORMATION:

APPLICANT: Bayer Aktiengesellschaft

APPLICANT: Hagen, Gustav

APPLICANT: Wick, Mareisa

APPLICANT: Zubov, Dmitry

TITLE OF INVENTION: Regulatory DNA Sequences of the Gene for the Human Catalytic

FILE REFERENCE: Telomerase Subunit, and Their Diagnostic and Therapeutic Use

CURRENT APPLICATION NUMBER: US/10/840,455

PRIOR FILING DATE: 2004-05-06

PRIOR APPLICATION NUMBER: PCT/EP98/08216

PRIOR FILING DATE: 1998-12-22

PRIOR APPLICATION NUMBER: US 09/582,246

PRIOR FILING DATE: 2000-09-21

PRIOR APPLICATION NUMBER: DE19757984.1

PRIOR FILING DATE: 1997-12-24

NUMBER OF SEQ ID NOS: 44

SOFTWARE: PatentIn version 3.2

SEQ ID NO 43

LENGTH: 26414

TYPE: DNA

ORGANISM: Homo sapiens

US-10-840-455-43

Query Match 97.2%; Score 972.8; DB 8; Length 26414;

Best Local Similarity 99.5%; Pred. No. 7.9e-286;

Matches 997; Conservative 0; Mismatches 2; Indels 3; Gaps 2;

Qy 1 GGCCTGGGATTTACAGGACCCGCCACCATGCGCCAGCTAAATTTTGTATTTTGTAGTAGAGA 60

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Qy 61 CGCGGGTGGGGGTTTCAACATGTTGGCCAGGCTGGTCTCGAACTTCTGAACTTCTGAACTCAGA 120

Db 9290 CGGGGGT--GGTGGGGTTTCAACATGTTGGCCAGGCTGGTCTCGAACTTCTGAACTCAGA 9347

Qy 121 TGATCCACCTGCTCTGCTCTCTTAAAGTGTCTGGGATTTACAGGCTGTAGGCCACCATGCCCCA 180

Db 9348 TGATCCACCTGCTCTGCTCTCTTAAAGTGTCTGGGATTTACAGGCTGTAGGCCACCATGCCCCA 9407

Qy 181 GCTCAGAAATTTTACTCTGTTTGTAGAAACATCTGGGCTCTGAGGTAGGAAGCTCACCCACTCA 240

Db 9408 GCTCAGAAATTTTACTCTGTTTGTAGAAACATCTGGGCTCTGAGGTAGGAAGCTCACCCACTCA 9467

Qy 241 AGTGTGCTGCTGTTTAAAGCAATGATAGAAATTTTATTTGTTGTTAGAACACTCTTGA 300

Db 9468 AGTGTGCTGCTGTTTAAAGCAATGATAGAAATTTTATTTGTTGTTAGAACACTCTTGA 9527

Qy 301 TGTTTACACTGTGATGACTAAGACATCATCAGCTTTTCAAAGACACACTAACTGACACC 360

Db 9528 TGTTTACACTGTGATGACTAAGACATCATCAGCTTTTCAAAGACACACTAACTGACACC 9587

Qy 361 ATAATCTCGGGTCTCTCTGGGATTCAGCGATCTTCATTTGAATGCCGGAGGGGTTTCC 420

Db 9588 ATAATCTCGGGTCTCTCTGGGATTCAGCAATCTTCATTTGAATGCCGGAGGGGTTTCC 9647

Qy 421 TCGCCATGCACATGCTTAAATTTACTCCAGCATAACTCTTCTGCTTCAATTTCTCTCTTC 480

Db 9648 TCGCCATGCACATGCTTAAATTTACTCCAGCATAACTCTTCTGCTTCAATTTCTCTCTTC 9707

Qy 481 CTCTTTTAAATTTGTTTCTTATGTTGGCTTCTCTGAGAGAACCAAGTGTAGAGTACA 540

Db 9708 CTCTTTTAAATTTGTTTCTTATGTTGGCTTCTCTGAGAGAACCAAGTGTAGAGTACA 9767

Qy 541 ACTTAACCTTTGTTGGAAACAAATTTTCCAAACCCGCCCTTTGCCCTTAGTGCGAGACAA 600

Db 9768 ACTTAACCTTTGTTGGAAACAAATTTTCCAAACCCGCCCTTTGCCCTTAGTGCGAGACAA 9827

Qy 601 TTCACAAACACAGCCCTTTTAAAGAGCTTAGGGATCACTAAGGGGATTTCTAGAAAGCG 660

Db 9828 TTCACAAACACAGCCCTTTTAAAGAGCTTAGGGATCACTAAGGGGATTTCTAGAAAGCG 9887

Qy 661 ACCCGTAATCTTAAGTATTTTACAAGACGAGCTTAACCTTCCAGCGAGGCTGACACCCAGG 720

Db 9888 ACCTGTAATCTTAAGTATTTTACAAGACGAGGCTTAACCTTCCAGCGAGGCTGACACCCAGG 9947

Qy 721 GAGGGTCGAGGCTGTTCAAATGCTAGCTTCCATTAATTAAGCAATTTCTCCGGCAGTT 780

Db 9948 GAGGGTCGAGGCTGTTCAAATGCTAGCTTCCATTAATTAAGCAATTTCTCCGGCAGTT 10007

Qy 781 TCTGAAAGTAGGAAGGTTACATTTAAGTTGCGTTTGTAGCAATTTCAAGTGTGCGGA 840

Db 10008 TCTGAAAGTAGGAAGGTTACATTTAAGTTGCGTTTGTAGCAATTTCAAGTGTGCGGA 10067

Qy 841 CCTCAGCTACAGCATCCTTGAAGGCTTCCGGAGACCCAGAGTTTCTCG-CCCTTTAGA 899

Db 10068 CCTCAGCTACAGCATCCTTGAAGGCTTCCGGAGACCCAGAGTTTCTCG-CCCTTTAGA 10127

Qy 900 TCGAACTTGAGCAACCCGGAGTCTGATTTCTGGGAAGTCTCCTCAGCTGCTCGGGTTG 959

Db 10128 TCGAACTTGAGCAACCCGGAGTCTGATTTCTGGGAAGTCTCCTCAGCTGCTCGGGTTG 10187

Qy 960 TCGCGGGCCCCAGGCTCTGGAGGGGACCACTGGCCGCTGTGGC 1001

Db 10188 TCGCGGGCCCCAGGCTCTGGAGGGGACCACTGGCCGCTGTGGC 10229

RESULT 14
US-09-733-294A-30
Sequence 30, Application US/09733294A
Patent No. US20020045588A1
GENERAL INFORMATION:
APPLICANT: Brett P. Monia
APPLICANT: William M. Gaarde
APPLICANT: Susan M. Freier
APPLICANT: Edward V. Wanciewicz
TITLE OF INVENTION: ANTISENSE MODULATION OF TERT EXPRESSION
FILE REFERENCE: ISPH-0527
CURRENT FILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: 09/572,423
PRIOR FILING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 108
SEQ ID NO 30
LENGTH: 51552
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: exon
LOCATION: (1)...(11492)
OTHER INFORMATION: exon 1
NAME/KEY: intron
LOCATION: (11493)...(11596)
OTHER INFORMATION: intron 1
NAME/KEY: exon
LOCATION: (11597)...(12950)
OTHER INFORMATION: exon 2
NAME/KEY: intron
LOCATION: (12951)...(21566)
OTHER INFORMATION: intron 2
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LOCATION: (21567)...(21762)
OTHER INFORMATION: exon 3
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LOCATION: (21763)...(23851)
OTHER INFORMATION: intron 3
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LOCATION: (23852)...(24032)
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LOCATION: (24720)...(24899)
OTHER INFORMATION: exon 5
NAME/KEY: intron
LOCATION: (24900)...(25393)
OTHER INFORMATION: intron 5
NAME/KEY: exon
LOCATION: (25394)...(25549)
OTHER INFORMATION: exon 6
NAME/KEY: intron
LOCATION: (25550)...(30196)
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NAME/KEY: exon
LOCATION: (30195)...(30292)
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LOCATION: (30293)...(31272)
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NAME/KEY: exon
LOCATION: (31273)...(31358)
OTHER INFORMATION: exon 8
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LOCATION: (31359)...(33843)
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NAME/KEY: unsure
LOCATION: 31450

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OTHER INFORMATION: intron 11
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LOCATION: (41875)...(42001)
OTHER INFORMATION: exon 12
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NAME/KEY: exon
LOCATION: (47036)...(47173)
OTHER INFORMATION: exon 15
NAME/KEY: intron
LOCATION: (47174)...(47709)
OTHER INFORMATION: intron 15
NAME/KEY: exon
LOCATION: (47710)...(50544)
OTHER INFORMATION: exon 16
US-09-733-294A-30

Query Match 97.2%; Score 972.8; DB 3; Length 51552;
Best Local Similarity 99.5%; Pred. No. 1.1e-285;
Matches 997; Conservative 0; Mismatches 2; Indels 3; Gaps 2;
QY 1 GGCTGGGATTACAGGCACCCGCCACCATGCCAGCTAATTTTGTATTTTAGTAGAGA 60
Db 9230 GGCTGGGATTACAGGCACCCGCCACCATGCCAGCTAATTTTGTATTTTAGTAGAGA 9289
QY 61 CGGGGGTGGGGTGGGGTTCACCATGTTGGCCAGCTGCTCGAACTTCGACCTCAGA 120
Db 9290 CGGGGGT--GGGTGGGGTTCACCATGTTGGCCAGCTGCTCGAACTTCGACCTCAGA 9347
QY 121 TGATCCACTGCTCTGCTCTCTAAAGTGTGGGATTACAGGTGTGAGCCACCATGCCCA 180
Db 9348 TGATCCACTGCTCTGCTCTCTAAAGTGTGGGATTACAGGTGTGAGCCACCATGCCCA 9407
QY 181 GCTCAGAAATTACTCTGTTTGAAGAAACATCTGGGTCTGAGGTAGGAAGCTCACCCACTCA 240
Db 9408 GCTCAGAAATTACTCTGTTTGAAGAAACATCTGGGTCTGAGGTAGGAAGCTCACCCACTCA 9467
QY 241 AGTGTGTGGTGTGTTTAAAGCCAAATCAGAAATTTTATTTTGTAGAACACTCTTGA 300
Db 9468 AGTGTGTGGTGTGTTTAAAGCCAAATCAGAAATTTTATTTTGTAGAACACTCTTGA 9527
QY 301 TGTTTTACACTGTGATGACTAAGACATCATCAGCTTTTCAAGACACACTTAACGACCC 360

Db 9528 TGTTTTACATGATGACCTAAGACATCATCAGCTTTTCAAGACACACTAATGACACC 9587
Qy 361 ATAAATCTGGGGTGTCTTCTGGGATCAGGATCTTCATTGAATGCGGGAGGCGTTTCC 420
Db 9588 ATAAATCTGGGGTGTCTTCTGGGATCAGGATCTTCATTGAATGCGGGAGGCGTTTCC 9647
Qy 421 TCGCATGACATGGTGTAAATTAATCTCAGCATATCTTCTGCTTCAATTTCTTCTTTC 480
Db 9648 TCGCATGACATGGTGTAAATTAATCTCAGCATATCTTCTGCTTCAATTTCTTCTTTC 9707
Qy 481 CCTCTTTTAAATTTGTGTTTCTATGTTGGCTTCTGCGAGAGAACAGTGAAGTACA 540
Db 9708 CCTCTTTTAAATTTGTGTTTCTATGTTGGCTTCTGCGAGAGAACAGTGAAGTACA 9767
Qy 541 ACTTAATCTTTGTTGGAAACAAATTTTCCAAACGCCCTTTGCGCTAGTGGCAGAGCAA 600
Db 9768 ACTTAATCTTTGTTGGAAACAAATTTTCCAAACGCCCTTTGCGCTAGTGGCAGAGCAA 9827
Qy 601 TTCACAAACACAGCCCTTTTAAAGGCTTAAAGGATCACTAAGGGGATTTCTAGNAGCG 660
Db 9828 TTCACAAACACAGCCCTTTTAAAGGCTTAAAGGATCACTAAGGGGATTTCTAGNAGCG 9887
Qy 661 ACCGTAATCTCTAGTATTTTACAGACAGGCTAACTTCCAGCGAGCGTGACGCCAGG 720
Db 9888 ACCGTAATCTCTAGTATTTTACAGACAGGCTAACTTCCAGCGAGCGTGACGCCAGG 9947
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Qy 781 TCTGAAGTAGGAAGGTACATTTAAGTTTGGTTTGTAGCATTTTCACTGTTTGCCTGA 840
Db 10008 TCTGAAGTAGGAAGGTACATTTAAGTTTGGTTTGTAGCATTTTCACTGTTTGCCTGA 10067
Qy 841 CCTCAGCTACAGCATCCTGCAAGGCTTCGGAGACCCAGAGTTTCTCG-CCCTTTAGA 899
Db 10068 CCTCAGCTACAGCATCCTGCAAGGCTTCGGAGACCCAGAGTTTCTCGCCCTTTAGA 10127
Qy 900 TCCAAACTTGAGCAACCCGAGTCTGATTCCTGGGAAAGTCTCAGCTGCTCGCGTTG 959
Db 10128 TCCAAACTTGAGCAACCCGAGTCTGATTCCTGGGAAAGTCTCAGCTGCTCGCGTTG 10187
Qy 960 TCGCGGGGCCCGCAGTCTGAGGGGACAGTGGCGGTGTGGC 1001
Db 10188 TCGCGGGGCCCGCAGTCTGAGGGGACAGTGGCGGTGTGGC 10229

RESULT 15

US-10-877-124-6

; Sequence 6, Application US/10877124

; Publication No. US20040242529A1

; GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.

; Lingner, Joachim

; Nakamura, Toru

; Chapman, Karen B.

; Morin, Gregg B.

; Harley, Calvin B.

; Andrews, William H.

; TITLE OF INVENTION: Human Telomerase Catalytic Subunit

; NUMBER OF SEQUENCES: 727

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, Eighth Floor

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/877,124

FILING DATE: 24-Jun-2004

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/432,503

FILING DATE: 02-Nov-1999

APPLICATION NUMBER: 08/974,549

FILING DATE: <Unknown>

APPLICATION NUMBER: US/08/844,419

FILING DATE: 18-Apr-1997

APPLICATION NUMBER: US/08/846,017

FILING DATE: 25-Apr-1997

APPLICATION NUMBER: US/08/851,843

FILING DATE: 06-May-1997

APPLICATION NUMBER: US/08/854,050

FILING DATE: 09-May-1997

APPLICATION NUMBER: US/08/911,312

FILING DATE: 14-Aug-1997

APPLICATION NUMBER: US/08/912,951

FILING DATE: 14-Aug-1997

APPLICATION NUMBER: US/08/915,503

FILING DATE: 14-Aug-1997

APPLICATION NUMBER: WO PCT/US97/17618

FILING DATE: 01-Oct-1997

APPLICATION NUMBER: WO PCT/US97/17885

FILING DATE: 01-Oct-1997

ATTORNEY/AGENT INFORMATION:

NAME: Apple, Randolph Ted

REGISTRATION NUMBER: 36,429

REFERENCE/DOCKET NUMBER: 015389-002610US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 4335 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

FEATURE:

NAME/KEY: -

LOCATION: 1..4335

OTHER INFORMATION: /note= "genomic DNA insert of pGRN144"

FEATURE:

NAME/KEY: intron

LOCATION: 2715..2818

OTHER INFORMATION: /note= "intron 1"

FEATURE:

NAME/KEY: intron

LOCATION: 4173..4326

OTHER INFORMATION: /note= "intron 2"

SEQUENCE DESCRIPTION: SEQ ID NO: 6:

US-10-877-124-6

Query Match 93.0%; Score 930.8; DB 8; Length 4335;
Best Local Similarity 99.1%; Pred. No. 2.2e-273;
Matches 999; Conservative 0; Mismatches 2; Indels 7; Gaps 6;
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Qy 61 CGGGGGTGGGGTGGGGTTCCACCATGTTGGCCAGGCTGGTCTCGAACTTCTGACCTCAGA 120
Db 498 CGGGGGTGGGGTGGGGTTCCACCATGTTGGCCAGGCTGGTCTCGAACTTCTGACCTCAGA 557
Qy 121 TGATCCACCTGCTCTGCTCTCTAAAGTGTGGGATTTACAGGTGTGAGCCACCATGCCCA 180
Db 558 TGATCCACCTGCTCTGCTCTCTAAAGTGTGGGATTTACAGGTGTGAGCCACCATGCCCA 617

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618 GCTCAGAAATTACTCTGTTTAGAAACATCTGGGTCTGAGGTAGGAAGCTCACCCACTCA 677
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QY 361 ATAATACCTGGGTGTCTTCTGGGTATCAGCGATCTTCAATGAATGCCGGGAGGGTTC 420
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798 ATAATACCTGGGTGTCTTCTGGGTATCAGCGATCTTCAATGAATGCCGGGAGGGTTC 857
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1098 ACCCGTAATCC-TAAGTATTTACAGACGAGGCTAACTCCAGCGAGCGTGACAGCCCGAG 1157
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Search completed: January 10, 2006, 20:35:11
Job time : 952.333 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 10, 2006, 11:12:13 ; Search time 210.333 Seconds
(without alignments)
3469.703 Million cell updates/sec

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Perfect score: 1001
Sequence: 1 ggcctgggattacagccacc.....gggaccagtggcgtggc 1001

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4637633 seqs, 364532575 residues

Total number of hits satisfying chosen parameters: 9275266

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA New:
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2: /cgm2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
3: /cgm2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
4: /cgm2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
5: /cgm2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
6: /cgm2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
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8: /cgm2_6/ptodata/1/pubpna/US13_NEW_PUB.seq.*
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10: /cgm2_6/ptodata/1/pubpna/US15_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	131	13.1	130472	6	US-10-995-561-13312
3	129.8	13.0	146656	7	US-11-121-086-68
4	128.4	12.8	167116	7	US-11-121-086-44
5	128	12.8	14670	6	US-10-995-561-13328
6	128	12.8	18895	6	US-10-995-561-13329
7	127.8	12.8	110711	6	US-10-995-561-13264
8	127.6	12.7	153142	7	US-11-121-086-27
9	127.6	12.7	203467	7	US-11-121-086-50
10	127	12.7	319608	7	US-11-145-492-1
11	127	12.7	319608	7	US-11-145-703-1
12	126.6	12.6	16843	6	US-10-995-561-13302
13	126.6	12.6	18238	6	US-10-995-561-13386
14	126.2	12.6	201	6	US-10-995-561-133560
15	125.8	12.6	175023	7	US-11-121-086-18
16	125.4	12.5	168556	7	US-11-112-908-59
17	125.4	12.5	170285	7	US-11-112-908-58
18	125.4	12.5	180862	7	US-11-112-908-40
19	125.2	12.5	40644	6	US-10-995-561-13480
20	124.8	12.5	159497	7	US-11-112-908-61
21	124.8	12.5	165857	7	US-11-121-086-34
22	124.8	12.5	171427	7	US-11-112-908-60
23	124.6	12.4	98716	6	US-10-995-561-13331

24	124.4	12.4	195998	6	US-10-995-561-13489
c 25	124.4	12.4	1080000	6	US-10-928-446A-1
c 26	124.4	12.4	1080000	6	US-10-928-446A-181
c 27	124.4	12.4	1080000	6	US-10-928-446A-183
c 28	124.4	12.4	1080000	6	US-10-928-446A-185
c 29	124.4	12.4	1080000	6	US-10-928-446A-187
c 30	124.4	12.4	1080000	6	US-10-928-446A-189
c 31	124.4	12.4	1080000	6	US-10-928-446A-191
c 32	124.4	12.4	1080000	6	US-10-928-446A-193
c 33	124.4	12.4	1080000	6	US-10-928-446A-195
c 34	124.4	12.4	1080000	6	US-10-928-446A-197
c 35	124.4	12.4	1080000	6	US-10-928-446A-199
c 36	124.4	12.4	1080000	6	US-10-928-446A-201
37	124.2	12.4	161994	7	US-11-112-908-57
38	123.8	12.4	125594	6	US-10-658-986-5
39	123.6	12.3	201990	6	US-10-995-561-13303
40	123.4	12.3	159138	6	US-10-995-561-13230
c 41	123	12.3	120697	7	US-11-121-086-48
c 42	123	12.3	175416	7	US-11-121-086-43
43	122.8	12.3	137000	6	US-10-515-538-11
44	122.2	12.2	201	6	US-10-995-561-13366
45	122.2	12.2	67126	6	US-10-995-561-13342

ALIGNMENTS

RESULT 1
US-11-121-086-73
; Sequence 73, Application US/11121086
; Publication No. US2005026459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121.086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 73
; LENGTH: 152335
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-73

Query Match	13.3%	Score 132.8;	DB 7;	Length 152335;
Best Local Similarity	81.1%	Pred. No. 5.9e-30;		
Matches 167;	Conservative 0;	Mismatches 37;	Indels 2;	Gaps 1;
QY	2	GCTGGATTACAGGCACCCGCCACATGCCAGCTAA--TTTTTGTATTTTAGTAGAG 59		
Db	84893	GCTGGATTATTAAGCACCCTGCCACCATGCCAGCTAAATTTTGTATTTTAGTAGAG 84952		
QY	60	ACGGGGTGGGGTGGGCTTACCATGTGGCCAGGCTGCTCGAACTTCGACCTCAG 119		
Db	84953	ACAAATGGGTATATGGGTTTACCATGTGGCCAGGTTGGTCTCGAACTTCGACCTCAG 85012		
QY	120	ATGATCCACCTGCCTCTGCCTCTTAAAGTGTGGGATTACAGGTGTGAGCCACCATGCC 179		
Db	85013	GTGATCCACCTGCCTCTGCCTCTTAAAGTGTGGGATTACAGGTGTGAGCCACCTGCC 85072		
QY	180	AGCTCAGAAATTACTCTCTTTAGAAA 205		
Db	85073	AGCCGATTACTGTAGTTTTATAGTAA 85098		

RESULT 2
US-10-995-561-13312
; Sequence 13312, Application US/10995561
; Publication No. US20050272054A1


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Db 3515 GCTGGGATTACAGGACCCGCCACCGCCGGCTCAATTTTGTATTTTAGTAGAGAC 3574
Qy 62 GGGGGTGGGGTGGGGTTCACCATTTGGCCAGGCTGGTCTCGAACTTCTGACCTCAGAT 121
Db 3575 GGGGGT-----TTACCATGTTGGCCAGGCTGGTCTCGAACTTCTGACCTCAGGT 3624
Qy 122 GATCCACCTGCTCTGCTCTCTAAAGTGTGGGATTACAGGTGTGAGCCACCATGCCAG 181
Db 3625 GATCCACCGCTAGGCTCTCCAAAGTGTGGGATACAGGTGTGAGCCACCGGCCGG 3684
Qy 182 CTCA 185
Db 3685 CTTA 3688

RESULT 6
US-10-995-561-13329/c
; Sequence 13329, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13329
; LENGTH: 18895
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-13329

Query Match 12.8%; Score 128; DB 6; Length 18895;
Best Local Similarity 85.3%; Pred. No. 5.5e-29;
Matches 157; Conservative 1; Mismatches 16; Indels 10; Gaps 1;

Qy 2 GCTGGGATTACAGGACCCGCCACCGCCGGCTCAATTTTGTATTTTAGTAGAGAC 61
Db 17066 GCTGGGATTACAGGACCCGCCACCGCCGGCTCAATTTTGTATTTTAGTAGAGAC 17007

Qy 62 GGGGGTGGGGTGGGGTTCACCATTTGGCCAGGCTGGTCTCGAACTTCTGACCTCAGAT 121
Db 17006 GGGGGT-----TTACCATGTTGCCAGGCTGGTCTCGAACTTCTGACCTCAGGT 16957

Qy 122 GATCCACCTGCTCTGCTCTCTAAAGTGTGGGATTACAGGTGTGAGCCACCATGCCAG 181
Db 16956 GATCCACCGCTAGGCTCTCCAAAGTGTGGGATACAGGTGTGAGCCACCGGCCGG 16897

Qy 182 CTCA 185
Db 16896 CTTA 16893

RESULT 7
US-10-995-561-13264
; Sequence 13264, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13264
; LENGTH: 110711
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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(110711)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-995-561-13264

Query Match 12.8%; Score 127.8; DB 6; Length 110711;
Best Local Similarity 81.4%; Pred. No. 1.8e-28;
Matches 162; Conservative 2; Mismatches 24; Indels 11; Gaps 1;

Qy 2 GCTGGGATTACAGGACCCGCCACCATGCCAGCTAAATTTTGTATTTTAGTAGAGAC 61
Db 32714 GCTGGGATTACAGGACATGCCACCATGCCGGCTAAATTTTGTATTTTAGTAGAGAC 32773

Qy 62 GGGGGTGGGGTGGGGTTCACCATTTGGCCAGGCTGGTCTCGAACTTCTGACCTCAGAT 121
Db 32774 -----AGGGTTTCASCATGTTGGCCAGGCTGGTCTCGAACTTCTGACCTCAGT 32822

Qy 122 GATCCACCTGCTCTGCTCTCTAAAGTGTGGGATTACAGGTGTGAGCCACCATGCCAG 181
Db 32823 GATCCACCTGCTGGCTGCCAAAGTGTAGGATTACAGGTGTGAGCCACCATGCCAG 32882

Qy 182 CTCAGAAATTTACTCTGTTT 200
Db 32883 CTTACAGTAGTAATTTTTT 32901

RESULT 8
US-11-121-086-27/c
; Sequence 27, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 27
; LENGTH: 153142
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-27

Query Match 12.7%; Score 127.6; DB 7; Length 153142;
Best Local Similarity 80.6%; Pred. No. 2.5e-28;
Matches 166; Conservative 0; Mismatches 29; Indels 11; Gaps 1;

Qy 2 GCTGGGATTACAGGACCCGCCACCATGCCAGCTAAATTTTGTATTTTAGTAGAGAC 61
Db 102935 GCTGGGATTATAGGGCTGCGCCACCATGCCAGCTAAATTTTGTATTTTAGTAGAGAC 102876

Qy 62 GGGGGTGGGGTGGGGTTCACCATTTGGCCAGGCTGGTCTCGAACTTCTGACCTCAGAT 121
Db 102875 G-----GGGTTTCAATGTTGGCCAGGTTGGTCTTGAACCTCTGACCTCAGGT 102827

Qy 122 GATCCACCTGCTCTGCTCTCTAAAGTGTGGGATTACAGGTGTGAGCCACCATGCCAG 181
Db 102826 GATCCACCTGCTGGCTCTCAAAGTGTGGGATTACAGGTGTGAGCCACCATGCCAGT 102767

Qy 182 CTCAGAAATTTACTCTGTTTAGAAACA 207
Db 102766 CTCATTTTGTATTTTAAAGAGA 102741

RESULT 9
US-11-121-086-50/c
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; Sequence 50, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 50
; LENGTH: 203467
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-50

Query Match      12.7%; Score 127.6; DB 7; Length 203467;
Best Local Similarity 77.5%; Pred. No. 3e-28;
Matches 172; Conservative 0; Mismatches 39; Indels 11; Gaps 1;

QY      2 GCTGGGATTACAGGCACCGCCGACCATGTCGCCAGCTAATTTTGTATTTTAGTAGAGAC 61
Db      143904 GCTGGGATTACAGGTGCTGCGACACCGCCGCTAATTTTGTATTTTAGTAGAGAT 143845

QY      62 GGGGGTGGGGGTGGGTTTACCATGTTGGCCAGCGTGTCTCGAACTTCTGACCTCAGAT 121
Db      143844 G-----GGGTTTCACTATGTTGGCCAGCGTGTCTTGAACCTCTGACCTCAGGA 143796

QY      122 GATCCACTGCTCTGCTCTCTAAAGTCTGGGATTACAGTGTGAGCCACCATGCCAG 181
Db      143795 GATCCACCGCTCGGCTCTCCAAAGTCTGAGATTACAGCGTGAGCCACCGTGCCTGG 143736

QY      182 CTCAGAAATTTACTCTGTTTAGAAACATCTGGGTCTGAGGTAG 223
Db      143735 CCCCCATTTTTTTTTTTTATATTCATTTATTTCAGAGGGAG 143694

RESULT 10
US-11-155-492-1/c
; Sequence 1, Application US/11155492
; Publication No. US20050266479A1
; GENERAL INFORMATION:
; APPLICANT: Weissenbach, Jean
; APPLICANT: Hazan, Jamil
; TITLE OF INVENTION: CLONING, EXPRESSION AND CHARACTERIZATION OF THE SPGA
; TITLE OF INVENTION: GENE RESPONSIBLE FOR THE MOST COMMON FORM OF AUTOSOMAL
; TITLE OF INVENTION: DOMINANT SPASTIC PARAPLEGIA
; FILE REFERENCE: R-341894
; CURRENT APPLICATION NUMBER: US/11/155,492
; CURRENT FILING DATE: 2005-06-20
; PRIOR APPLICATION NUMBER: US/09/830,902
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: FR 99 11097
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: PCT/FR00/02433
; PRIOR FILING DATE: 2000-09-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn Vers. 2.0
; SEQ ID NO 1
; LENGTH: 110000
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: exon
; LOCATION: (9932) ... (10471)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (10472) ... (33718)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (89562) ... (89641)
;
; LOCATION: (33719) ... (33805)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (33806) ... (35748)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (35749) ... (35832)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (35833) ... (45022)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (45023) ... (45118)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (45119) ... (60863)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (60864) ... (61051)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (61052) ... (61927)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (61928) ... (62061)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (62062) ... (62344)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (62345) ... (62438)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (62439) ... (73173)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (73174) ... (73248)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (73249) ... (74633)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (74634) ... (74705)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (74706) ... (82788)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (82789) ... (82864)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (82865) ... (83102)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (83103) ... (83194)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (83195) ... (83334)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (83335) ... (83414)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (83415) ... (88129)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (88130) ... (88172)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (88173) ... (89561)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (89562) ... (89641)
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OTHER INFORMATION: 3'regulatory region g34872 gene
FEATURE:
NAME/KEY: exon
LOCATION: 215819..215941
OTHER INFORMATION: exon R complement g34872 gene
FEATURE:
NAME/KEY: exon
LOCATION: 215819..215975
OTHER INFORMATION: exon Rbis complement g34872 gene
FEATURE:
NAME/KEY: exon
LOCATION: 216661..216952
OTHER INFORMATION: exon Qbis complement g34872 gene
FEATURE:
NAME/KEY: exon
LOCATION: 217027..217061
OTHER INFORMATION: exon Q1 complement g34872 gene
FEATURE:
NAME/KEY: exon
LOCATION: 229647..229742
OTHER INFORMATION: exon X complement g34872 gene
FEATURE:
NAME/KEY: exon
LOCATION: 230408..230721
OTHER INFORMATION: exon P complement g34872 gene
FEATURE:
NAME/KEY: exon
LOCATION: 231272..231412
OTHER INFORMATION: exon Obis complement g34872 gene
FEATURE:
NAME/KEY: exon
LOCATION: 231787..231880
OTHER INFORMATION: exon O2 complement g34872 gene
FEATURE:
NAME/KEY: exon
LOCATION: 231870..231879
OTHER INFORMATION: exon O1 complement g34872 gene
FEATURE:
NAME/KEY: exon
LOCATION: 234174..234321
OTHER INFORMATION: exon O complement g34872 gene
FEATURE:
NAME/KEY: exon
LOCATION: 237406..237428
OTHER INFORMATION: exon Nbis complement g34872 gene
FEATURE:
NAME/KEY: exon
LOCATION: 239719..239807
OTHER INFORMATION: exon N2 complement g34872 gene
FEATURE:
NAME/KEY: exon
LOCATION: 239719..239853
OTHER INFORMATION: exon N complement g34872 gene
FEATURE:
NAME/KEY: exon
LOCATION: 240528..240569
OTHER INFORMATION: exon M1117 complement g34872 gene
FEATURE:
NAME/KEY: exon
LOCATION: 240528..240596
OTHER INFORMATION: exon M1090 complement g34872 gene
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NAME/KEY: exon
LOCATION: 240528..240617
OTHER INFORMATION: exon M1069 complement g34872 gene
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NAME/KEY: exon
LOCATION: 240528..240644
OTHER INFORMATION: exon MS2 complement g34872 gene
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NAME/KEY: exon
LOCATION: 240528..240824
OTHER INFORMATION: exon M862 complement g34872 gene
FEATURE:
NAME/KEY: exon
LOCATION: 240528..240994
OTHER INFORMATION: exon M692 complement g34872 gene
FEATURE:
NAME/KEY: exon
LOCATION: 240528..241685
OTHER INFORMATION: exon M1 complement g34872 gene
FEATURE:
NAME/KEY: exon
LOCATION: 240800..240993
OTHER INFORMATION: exon MS1 complement g34872 gene
FEATURE:
NAME/KEY: misc feature
LOCATION: 241686..243685
OTHER INFORMATION: 5'regulatory region g34872 gene
FEATURE:
NAME/KEY: misc feature
LOCATION: 290652..292652
OTHER INFORMATION: 3'regulatory region g34665 gene

Query Match 12.7%; Score 127; DB 7; Length 319608;
Best Local Similarity 85.8%; Pred. No. 5.9e-28;
Matches 157; Conservative 0; Mismatches 15; Indels 11; Gaps 1;

Qy 2 GCTGGGATTACAGCACCGCCACCATGCCAGCTAATTTTTTGTATTTTAGTAGAGAC 61
|||
Db 88523 GCTGGGATTACAGCACCGCCACCATGCCAGCTAATTTTTTGTATTTTAGTAGAGAC 88464
|||

Qy 62 GGGGGTGGGGTGGGGTTCCACCATGTTGGCCAGCGTGGTCTCGAACTTCTGACCTCAGAT 121
|||
Db 88463 -----TGGGTTTCACTATGTTAGCCAGCGTGGTCTTGAACCTTCTGATCTCAGGT 88415
|||

Qy 122 GATCCACCTGCTCTGCTCTCTAAAGTGGCTGGGATTACAGGTGTGAGCCACCATGCCAG 181
|||
Db 88414 GATCCACCATCTGGGCTCCCAAAGTGTGGGATTACAGGTGTGAGCCACCATGCCAG 88355
|||

Qy 182 CTC 184
Db 88354 CCC 88352

RESULT 12
US-10-995-561-13302
; Sequence 13302, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13302
; LENGTH: 16643
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(16643)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-995-561-13302

Query Match 12.6%; Score 126.6; DB 6; Length 16643;
Best Local Similarity 86.2%; Pred. No. 1.4e-28;
Matches 156; Conservative 0; Mismatches 14; Indels 11; Gaps 1;
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Search completed: January 10, 2006, 20:45:52
Job time : 216.333 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 10, 2006, 05:49:50 ; Search time 4711 Seconds

(without alignments)

9941.386 Million cell updates/sec

Title: US-09-615-039-1_COPY_11500_12500

Perfect score: 1001

Sequence: 1 ggcctgggattacaggaccaccc.....gggaccagtggcgtgtggc 1001

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_hc:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_g81:*
10: gb_g82:*
11: gb_g83:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	134.2	13.4	883	5	BQ687748 AGENCOURT
2	133.2	13.3	604	3	BM990713 UI-H-D10-
3	132.6	13.2	1035	3	BM807194 AGENCOURT
4	131.8	13.2	467	9	AQ349390 RPC111-12
5	131.6	13.1	528	7	CN263775 170004241
6	131.2	13.1	723	10	AG030984 Pan trogl
7	130.2	13.0	1025	3	BM907570 AGENCOURT
8	129.8	13.0	379	1	AA601673 no01f02.s
9	129.2	12.9	379	1	AI245348 qk28g06.x
10	129.2	12.9	427	1	AW514662 xu97f09.x
11	129.2	12.9	646	1	AW967131 EST379205
12	129	12.9	416	1	AV693536 AV693536
13	129	12.9	421	1	AV691556 AV691556
14	128.8	12.9	488	1	AA720582 rw21h01.s
15	128.8	12.9	603	3	BQ230374 AGENCOURT
16	128.8	12.9	635	2	BE908214 601500472
17	128.8	12.9	657	9	AQ473201 CITBI-EI-
18	128.8	12.9	671	9	AQ470937 CITBI-EI-
19	128.6	12.8	455	9	AQ392348 CITBI-EI-
20	128.6	12.8	490	9	AQ416174 RPC1-11-1
21	128.4	12.8	536	7	CK821280 ig51b10.x
22	128.4	12.8	578	3	BM314487 ig51b10.y

ALIGNMENTS

RESULT 1

BQ687748

LOCUS

DEFINITION

AGENCOURT 8186578 NIH_MGC_110 Homo sapiens

5', mRNA sequence.

ACCESSION

BQ687748

VERSION

BQ687748.1

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

REFERENCE

1 (bases 1 to 883)

AUTHORS

NIH-MGC http://mgc.nci.nih.gov/.

TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Rubin Laboratory

CDNA Sequencing by: The I.M.A.G.E. Consortium (ILNL)

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/ILNL at:

http://image.llnl.gov

Plate: LLCM2396 row: f column: 20

High quality sequence stop: 531.

Location/Qualifiers

1..883

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:6251539"

/tissue_type="ductal carcinoma, cell line"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH_MGC_110"

/note="Organ: pancreas; Vector: pOTB7; Site:1: XhoI; Site 2: EcoRI; CDNA made by oligo-dr priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

FEATURES

source

23	128.2	12.8	372	3	BM991270	BM991270 UI-H-D10-
24	128.2	12.8	445	1	AI497824	AI497824 tm89g10.x
25	128.2	12.8	674	5	BX501315	BX501315 DKF2p779C
26	128.2	12.8	854	6	CD171905	CD171905 AGENCOURT
27	128	12.8	894	5	BQ439884	BQ439884 AGENCOURT
28	128	12.8	1840	4	CR857550	CR857550 Pongo pyg
29	127.4	12.7	417	1	AV697609	AV697609 AV697609
30	127.4	12.7	571	9	AQ381323	AQ381323 RPC111-13
31	127.2	12.7	633	3	BM977586	BM977586 UI-CF-BN1
32	127	12.7	430	9	AQ393433	AQ393433 CITBI-EI-
33	126.6	12.6	361	9	AQ014345	AQ014345 RPC111-23
34	126.6	12.6	605	7	CR549909	CR549909 DKF2p4690
35	126.6	12.6	635	7	CN265093	CN265093 170004245
36	126.6	12.6	660	5	AQ014266	AQ014266 RPC111-23
37	126.6	12.6	767	5	BQ775984	BQ775984 UI-H-FH0-
38	126.6	12.6	1808	4	AF130050	AF130050 Homo sapi
39	126.6	12.6	2110	4	BC012538	BC012538 Homo sapi
40	126.4	12.6	288	9	AQ391637	AQ391637 CITBI-EI-
41	126.4	12.6	392	1	AA484892	AA484892 ne81f09.s
42	126.4	12.6	436	2	BF816190	BF816190 MR2-CI012
43	126.4	12.6	437	1	AA572921	AA572921 nm42h05.s
44	126.4	12.6	689	10	AG146015	AG146015 Pan trogl
45	126.2	12.6	311	6	CB230206	CB230206 AGENCOURT

ORIGIN

Query Match 13.4%; Score 134.2; DB 5; Length 883;
 Best Local Similarity 81.5%; Pred. No. 2.4e-19;
 Matches 172; Conservative 0; Mismatches 28; Indels 11; Gaps 1;
 QY 2 GCTGGATTACAGCAGCCGCCACCATGCTCCGAGCTGCTCGAATTTCTGATTTTGTAGTACGAC 61
 DB 237 GCTGGATTACAGCAGCCGCCACCATGCTCCGAGCTGCTCGAATTTCTGATTTTGTAGTACGAC 296
 QY 62 GGGGGTGGGGTGGGGTTTCCATGTTGGCCAGGCTGCTCGAATTTCTGATTTTGTAGTACGAC 121
 DB 297 A-----GGGTTTCCATGTTGGCCAGGCTGCTCGAATTTCTGATTTTGTAGTACGAC 345
 QY 122 GATCACCTGCTCTGCTCTCTAAAGTCTGGGATTACAGTGTGAGCCACCATGCCAG 181
 DB 346 GATCACCTGCTCTGCTCTCTAAAGTCTGGGATTACAGTGTGAGCCACCATGCCAG 405
 QY 182 CTCAGATTACTCTGTTTAAACAATCTGG 212
 DB 406 CCCTGAATTAATAATTTTAAATAAGTTGG 436

RESULT 2

BM990713
 LOCUS UI-H-D10-atr-m-07-0-UI.s1 NCI CGAP_D10 Homo sapiens cDNA clone
 DEFINITION IMAGE:5863470 3', mRNA sequence.

ACCESSION BM990713

VERSION BM990713.1 GI:19710102

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 604)

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Dr. Jose Mercuende

cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Clone distribution information can be found

through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

The following repetitive elements were found in this cDNA

sequence: 11-302, >ALU (matched complement) 218-325, >ALU (matched

complement)

Seq primer: M13 FORWARD

POLYA-Yes.

Location/Qualifiers

1. .604

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:5863470"

/tissue_type="Lung Focal Fibrosis"

/dev_stage="Adult"

/lab_host="NCI CGAP D10"

/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a

modified polylinker; Site 1: EcoR I; Site 2: Not I;

NCI CGAP D10 is a cDNA library containing the following

tissues(s): A pool of Lung Focal Fibrosis. The library was

constructed according to Bonaldo, Lennon and Soares,

Genome Research, 6:791-806, 1996. First strand cDNA

synthesis was primed with an oligo-dT primer containing a

Not I site. Double stranded cDNA was ligated to an EcoR I

adaptor, digested with Not I, and cloned directionally

into pT7T3-Pac vector. The oligonucleotide used to prime
 the synthesis of first-strand cDNA contains a library tag
 sequence that is located between the Not I site and the
 (drr)18 tail. The sequence tag for this library is
 ATACGGGGTC.

TAG TISSUE=lung with fibrosis

TAG LIB=UI-H-D10

TAG SEQ=ATACGGGGTC"

ORIGIN

Query Match 13.3%; Score 133.2; DB 3; Length 604;
 Best Local Similarity 74.4%; Pred. No. 4e-19;
 Matches 186; Conservative 0; Mismatches 53; Indels 11; Gaps 1;
 QY 2 GCTGGATTACAGCAGCCGCCACCATGCTCCGAGCTGCTCGAATTTCTGATTTTGTAGTACGAC 61
 DB 132 GCTGGATTACAGCAGCCGCCACCATGCTCCGAGCTGCTCGAATTTCTGATTTTGTAGTACGAT 191
 QY 62 GGGGGTGGGGTGGGGTTTCCATGTTGGCCAGGCTGCTCGAATTTCTGATTTTGTAGTACGAT 121
 DB 192 G-----GGGTTTCCATGTTGGCCAGGCTGCTCGAATTTCTGATTTTGTAGTACGAT 240
 QY 122 GATCCACCTGCTCTGCTCTCTAAAGTCTGGGATTACAGTGTGAGCCACCATGCCAG 181
 DB 241 GATCCGCCGCTCTGCGCTCCCAAAGTCTGGGATTACAGGCTGAGCCACCGGCCAG 300
 QY 182 CTGAGAAATTTACTCTCTGTTTAAACAATCTGGGCTGAGGTAGGAAGCTCAACCCACCTCAA 241
 DB 301 CCAAACCTTACTATTTTAAAGAATTTTCCAGAGTTTAAATTTCTGACATAGCTTAA 360
 QY 242 GTGTTGTGGT 251
 DB 361 GTTTCAGT 370

RESULT 3

BM807194/c

LOCUS BM807194

DEFINITION AGENCOURT_6566418 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:5738243

5', mRNA Sequence.

ACCESSION BM807194

VERSION BM807194.1 GI:19124010

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 1035)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: L1AM12749 row: k column: 12

High quality sequence stop: 675.

Location/Qualifiers

1. .1035

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:5738243"

/tissue_type="duodenal

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH MGC 88"

/note="Organ: small intestine; Vector: PCMV-SPORT6;

source

FEATURES

Site 1: NotI; Site 2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.767 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 13.2%; Score 132.6; DB 3; Length 1035;
 Best Local Similarity 79.5%; Pred. No. 5.4e-19;
 Matches 174; Conservative 0; Mismatches 34; Indels 11; Gaps 1;

QY 2 GCTGGGATTACAGGACCCGCCACATGCCAGCTAATTTTGTATTTTAGTAGAGAC 61
 DB CTTGGGATTACAGGACCTGCGCCATGCCAGCTAATTTTGTATTTTAGTAGAGAC 430

QY 62 GGGGGTGGGGTGGGGTTCACATGTTGGCCAGGCTGCTCGAACTTCTGACCTCAGAT 121
 DB GGGGGTGGGGTGGGGTTCACATGTTGGCCAGGCTGCTCGAACTTCTGACCTCAGAT 381

QY 122 GATCCACCTGCTGCTGCTCTAAAGTCTGGGATTACAGGTGTGAGCCACCATGCCAG 181
 DB GATCCACCTGCTGCTGCTCTAAAGTCTGGGATTACAGGTGTGAGCCACCATGCCAG 321

QY 182 CTCAGAAATTACTCTGTTTAGAAACATCTGGGCTGAGG 220
 DB CCAAAACTATTTTAAAGATATAAATGCTCACAG 282

RESULT 4
 LOCUS AQ349390
 DEFINITION RPC111-120M7.TJ RPC1-11 Homo sapiens genomic clone RPC1-11-120M7, genomic survey sequence.
 ACCESSION AQ349390
 VERSION AQ349390.1 GI:4174286
 KEYWORDS GSS.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 467)
 AUTHORS Zhao, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and Venter, J.C.
 TITLE Use of BAC End Sequences from Library RPC1-11 for Sequence-Ready Map Building
 JOURNAL Unpublished (1997)
 COMMENT Other GSSs: RPC111-120M7.TV
 Contact: Shaying Zhao, William Nierman, Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: hbe@tigr.org
 Clones are derived from the human BAC library RPC1-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering>) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tldb/humgen/bac_end_search/bac_end_search.html
 Seq primer: SP6
 Class: BAC ends.
 Location/Qualifiers
 1..467
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="GDB:754590"
 /db_xref="taxon:9606"
 /clone="RPC1-11-120M7"
 /sex="Male"
 /cell_type="Lymphocytes"
 /clone_lib="RPC1-11"
 /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;

RPC111 Human Male BAC Library"

ORIGIN

Query Match 13.2%; Score 131.8; DB 9; Length 467;
 Best Local Similarity 83.4%; Pred. No. 8.2e-19;
 Matches 166; Conservative 0; Mismatches 22; Indels 11; Gaps 1;

QY 2 GCTGGGATTACAGGACCCGCCACATGCCAGCTAATTTTGTATTTTAGTAGAGAC 61
 DB GCTGGGATTACAGGACCTGCGCCATGCCAGCTAATTTTGTATTTTAGTAGAGAC 320

QY 62 GGGGGTGGGGTGGGGTTCACATGTTGGCCAGGCTGCTCGAACTTCTGACCTCAGAT 121
 DB GGGGGTGGGGTGGGGTTCACATGTTGGCCAGGCTGCTCGAACTTCTGACCTCAGAT 369

QY 122 GATCCACCTGCTGCTGCTCTAAAGTCTGGGATTACAGGTGTGAGCCACCATGCCAG 181
 DB GATCCACCTGCTGCTGCTCTAAAGTCTGGGATTACAGGTGTGAGCCACCATGCCAG 429

QY 182 CTCAGAAATTACTCTGTTT 200
 DB CTAATTTATTTATTTT 448

RESULT 5
 LOCUS CN263775
 DEFINITION 17000424180545 GRN_EB Homo sapiens cDNA 5', mRNA sequence.
 ACCESSION CN263775
 VERSION CN263775.1 GI:47280189
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 528)
 AUTHORS Li, Y., Xu, C., Pang, R., Guegler, K., Rao, M.S., Mandalam, R., Lebkowek, J. and Stanton, L.W.
 TITLE Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation
 JOURNAL Nat. Biotechnol. 22 (6), 707-716 (2004)
 PUBMED 15146197
 COMMENT Contact: Brandenberger R
 Regenerative Medicine
 Geron Corporation
 230 Constitution Drive, Menlo Park, CA 94025, USA
 Tel: 650 473 8658
 Fax: 650 473 7760
 Email: rbrandenberger@geron.com
 Insert Length: 528 Std Error: 0.00.
 Location/Qualifiers
 1..528
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /tissue_type="embryonic stem cells, embryoid bodies derived from H1, H7 and H9 cells"
 /clone_lib="GRN_EB"
 /note="Oligo dT primed, full-length enriched cDNA library from embryoid body outgrowths derived from hES cell lines H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free conditions."

ORIGIN

Query Match 13.1%; Score 131.6; DB 7; Length 528;
 Best Local Similarity 81.0%; Pred. No. 9.1e-19;
 Matches 170; Conservative 0; Mismatches 29; Indels 11; Gaps 1;

QY 2 GCTGGGATTACAGGACCCGCCACATGCCAGCTAATTTTGTATTTTAGTAGAGAC 61
 DB GCTGGGATTACAGGTCGCCACCATGCCAGCTAATTTTGTATTTTAGTAAGAC 225

```

Qy 62 GGGGGTGGGGTGGGGTTCCACATGTTGGCAGGCTGGTCTCGAATCTTCTGACCTCAGAT 121
Db |-----GGGTTTCCACATGTTGGCAGGCTGGTCTTGAACCTCTGACCTCAGGT 274
Qy 122 GATCCACCTGCTCTGCTCTCTAAAGTGTGGGATTAACAGTGTGAGCCACCATGCCCGAG 181
Db |-----GGGTTTCCACATGTTGGCAGGCTGGTCTTGAACCTCTGACCTCAGGT 274
Qy 182 CTGAGAAATTTACTCTGTTTGAACATCTG 211
Db |-----GGGTTTCCACATGTTGGCAGGCTGGTCTTGAACCTCTGACCTCAGGT 274
Qy 335 CCCTGTCTTACTGTTAATGAATTTTGTG 364

RESULT 6
AG030984/c
LOCUS
DEFINITION Pan troglodytes DNA, clone: PTB-003114.R, genomic survey sequence.
ACCESSION AG030984
VERSION AG030984.1 GI:16557857
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Pan.
REFERENCE
1 Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
Unpublished
2 (bases 1 to 723)
Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:chimbep@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
clone tracking errors.
PRIMERS
Sequencing: M13Rev
LIBRARY
Vector : pKS145
R.Site 1 : SacI
R.Site 2 : SacI.
FEATURES
source
Location/Qualifiers
1..723
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-003114.R"
/sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"

ORIGIN
Query Match 13.1%; Score 131.2; DB 10; Length 723;
Best Local Similarity 81.2%; Pred. No. 1.1e-18;
Matches 169; Conservative 0; Mismatches 28; Indels 11; Gaps 1;

Qy 2 GCTGGGATTAACAGCACCGCCACCATGCCAGCTAATTTTGTATTTTAGTAGAGAC 61
Db |-----GGGTTTCCACATGTTGGCAGGCTGGTCTTGAACCTCTGACCTCAGGT 274
Qy 62 GGGGGTGGGGTGGGGTTCCACATGTTGGCAGGCTGGTCTCGAATCTTCTGACCTCAGAT 121
Db |-----GGGTTTCCACATGTTGGCAGGCTGGTCTTGAACCTCTGACCTCAGGT 274
Qy 377 G-----GGGTTTCCACATGTTGGCAGGCTGGTCTCGAATCTTCTGACCTCAGGT 329
Qy 122 GATCCACCTGCTCTGCTCTCTAAAGTGTGGGATTAACAGTGTGAGCCACCATGCCCGAG 181

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Db 328 GATCCACCGCTCTCAGCTCCCAAGTGTGGGATTAACAGTGTGAGCCACCATGCCCGAG 269
Qy 182 CTGAGAAATTTACTCTGTTTGAACATC 209
Db 268 CCTGAAATCTGCACCTTTTGACAAGCATC 241

RESULT 7
BM907570/c
LOCUS
DEFINITION BM907570 1025 bp mRNA linear EST 12-MAR-2002
5', mRNA sequence.
ACCESSION BM907570
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 (bases 1 to 1025)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: csapsb-remail.nih.gov
Tissue Procurement: DCTD/DTF/Gazdar
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12743 row: h column: 21
High quality sequence stop: 606.
FEATURES
source
Location/Qualifiers
1..1025
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5735876"
/tissue_type="large cell carcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_68"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.8 kb. Library constructed by Life
Technologies."
ORIGIN
Query Match 13.0%; Score 130.2; DB 3; Length 1025;
Best Local Similarity 81.2%; Pred. No. 1.9e-18;
Matches 168; Conservative 0; Mismatches 28; Indels 11; Gaps 1;

Qy 2 GCTGGGATTAACAGCACCGCCACCATGCCAGCTAATTTTGTATTTTAGTAGAGAC 61
Db 429 GCTGGGACTACAGCGCCACCATACCTGGCTAATTTTGTATTTTAGTAGAGAC 370
Qy 62 GGGGGTGGGGTGGGGTTCCACATGTTGGCAGGCTGGTCTCGAATCTTCTGACCTCAGAT 121
Db 369 AGGGT-----TTATCCATGTTGGCAGGCTGGTCTCAAACTCTGACCTCAAGT 321
Qy 122 GATCCACCTGCTCTGCTCTCTAAAGTGTGGGATTAACAGTGTGAGCCACCATGCCCGAG 181
Db 320 GATCTCTCTGCTCGGCTCCCAAGTGTGGGATTAACAGTGTGAGCCACCATGCCCGAG 261
Qy 182 CTGAGAAATTTACTCTGTTTGAACATC 208
Db 260 CCAATAATTTCTCGATATAATAAAAT 234

RESULT 8

```

AA601673/c	AA601673	379 bp	mrna	linear	EST 01-OCT-1997
LOCUS	no01f02.s1	NCI_CGAP Phel	Homo sapiens	cdna	IMAGE:1099419 3'
DEFINITION		similar to contains Alu repetitive element;; mRNA sequence.			
ACCESSION	AA601673				
VERSION	AA601673.1	GI:2435298			
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	1 (bases 1 to 379)				
TITLE	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .				
JOURNAL	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index				
COMMENT	Unpublished (1997) Contact: Robert Strausberg, Ph.D. Email: cgapbs@mail.nih.gov Tissue Procurement: W. Marston Linehan, M.D., Michael R. Emmert-Buck, M.D., Ph.D. cdna Library Preparation: Stratagene, Inc. cdna Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html Insert Length: 1018 Std Error: 0.00 Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 373. Location/Qualifiers 1..379 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clones="IMAGE:1099419" /tissue_type="pheochromocytoma" /lab_host="SOLR (kanamycin resistant)" /clone_lib="NCI_CGAP_Phel" /note="Vector: Bluescript SK-; Site 1: EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo dr. Pheochromocytoma. 5' adaptor sequence: 5' GAATTCGGCAGG 3' 3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3' Average insert size: 1.3 kb."				
FEATURES	source				
ORIGIN	Query Match 13.0%; Score 129.8; DB 1; Length 379; Best Local Similarity 69.1%; Pred. No. 2.3e-18; Matches 197; Conservative 0; Mismatches 77; Indels 11; Gaps 1; Qy 2 GCTGGGATTACAGGCACCGCCACCATGCCCCAGCTAAATTTTCTGATTTTGTAGTAGAC 61 Db 374 GCTGGGATTACAGGCACCGCCACCATGCCCCAGCTAAATTTTGTATTTTGTAGTAGAC 315 Qy 62 GGGGGTGGGGTGGGGTTCACCATGTTGGCCAGGCTGGTCTCGAACTTCTGACCTCAGAT 121 Db 314 -----AGGGTTTCGCCATGTTGGCCAGTGGTCTCGAACTCTCGACCTCAGGA 266 Qy 122 GATCCACTGCTCTGCTCTCTAAAGTCTGGGATTACAGGTGTGAGCCACATGCCCGAG 181 Db 265 GATCCACCTGCTTCAGCTCTCCAAGTGTGGGATTACAGCGGTGAGCCACCGGCCCGAG 206 Qy 182 CTCAGAAATTTCCTGTTTGTAGAAACATCTGGGTCTGAGGTAGGAAGCTCACCCCACTCAA 241 Db 205 CCTACAGCCTAATCTATATGTGCTCAATGCTGTAGTGTGCTCATTTGTTCTAGGCT 146 Qy 242 GTGTTGTGGTGTGTTTAAAGCCCAATAGTAAATTTTTTTTATGTTGT 286 Db 145 TTTCACTGAAGAGCTTAAGAGCTAGAAAACACACTTTTTTTTTTTT 101				

```

LOCUS       AI245348               379 bp    mRNA          linear      EST 28-JAN-1999
DEFINITION  qk28g06.x1 NCI_CGAP Kid3 Homo sapiens cDNA clone IMAGE:1870330 3'
            similar to contains Alu repetitive element;; mRNA sequence.
ACCESSION   AI245348
VERSION     AI245348.1 GI:3840745
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE   1 (bases 1 to 379)
AUTHORS    NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
JOURNAL     Unpublished (1997)
COMMENT    Contact: Robert Strausberg, Ph.D.
            Email: cgapsb-xemail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert length: 559 Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 364.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:1870330"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP Kid3"
                     /note="Organ: kidney; Vector: pTTT3D-Pac (Pharmacia) with
                     a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer,
                     double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not
                     I and Eco RI sites of the modified pTTT3 vector. mRNA
                     source: 2 pooled kidneys. Library went through one round
                     of normalization. Library constructed by Bento Soares and
                     M. Fatima Bonaldo."
ORIGIN
Query Match      12.9%; Score 129.2; DB 1; Length 379;
Best Local Similarity 86.8%; Pred. No. 3.1e-18;
Matches 158; Conservative 0; Mismatches 13; Indels 11; Gaps 1;

QY  1  GGCTGGGATTACAGGACCGCCACCATGCCAGCTAAATTTTGTATTTTGTAGTAGAGA  60
    |||
DB  116 GGCTGGGATTACAGGCGATGGCCACCATGCCCGGCTAAATTTTGTATTTTGTAGTAGAGA  175
    |||
QY  61  CGGGGGTGGGGGCTGGGGCTTACCATGTGTGGCCAGCGTGGTCTCGAACTTCTGACCTCAGA  120
    |||
DB  176 CG-----GGGTTTACCATGTGTGGCCAGCGTGGTCTCGAACTTCTGACCTCAGG  224
    |||
QY  121 TGATCCACCTGCCTCTGCCTCTTAAAGTGTGGGATTACAGGTGTGAGCCACCATGCCCCA  180
    |||
DB  225 TGGTCCACCTGCCTCAGCCTCCGAAGGTGCTGGGATTACAGGCGTGAGCCACCATGCCCCA  284
    |||
QY  181 GC 182
    ||
DB  285 GC 286

RESULT 10
AWS14662/c
LOCUS       AWS14662
DEFINITION  xu97f09.x1 NCI CGAP Ut2 Homo sapiens cDNA clone IMAGE:2809673 3'

```

DD	445	TTTCTAGTGGAGGCTTAAAGAGCTAAGAGGACACCTTTTTTTTTTT	101
<hr/>			
RESULT 9			
AT245348			
LOCUS	AW514662/c		
DEFINITION	RESULT 10		

similar to contains Alu repetitive element,, mRNA sequence.

ACCESSION AW514662
 VERSION AW514662.1 GI:7152744
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 427)
 AUTHORS NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaps-remail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Greg Lennon, Ph.D.
 Clone distribution: Washington University Genome Sequencing Center
 found through the I.M.A.G.E. Consortium/LINL at: image.llnl.gov/image/html/iresources.shtml
 Seq primer: -40UP from Gibco
 High quality sequence stop: 399.

FEATURES
 source Location/Qualifiers
 1..427
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2809673"
 /tissue_type="moderately-differentiated endometrial adenocarcinoma, 3 pooled tumors"
 /lab_host="DH10B"
 /clone_lib="NCI CGAP Ut2"
 /note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.85 Kb. Life Technologies catalog #: 11539-012"

ORIGIN
 Query Match 12.9%; Score 129.2; DB 1; Length 427;
 Best Local Similarity 81.1%; Pred. No. 3.1e-18;
 Matches 167; Conservative 0; Mismatches 28; Indels 11; Gaps 1;
 2 GCTGGGATTACAGCACCACCGCCACCATGCCAGCTAATTTTGTATTTTAGTAGAGAC 61
 215 GCTGGGACTACAGCACCACCGCCACCATGCCAGCTAATTTTGTATTTTAGTAGAGAT 156
 62 GGGGGTGGGGTGGGGTTACCATGTTGGCCAGGCTGGTCTCGAAGTCTTGACCTCAGAT 121
 155 GA-----GGTTTCACCATTTTGGCCAGGCTGATCTGCAACTCTCTGACCTCAGGT 107
 122 GATCCACCTGCTGCTCTCTTAAGTCTGGGATTACAGTGTGACCCACCATGCCCGAG 181
 106 GATCCACCGCTCAGGCTCCCAAGTCTGGGATTACAGTGTGAGCCACACCCCGG 47
 182 CTCAGAAATTTACTCTGTTTGAACA 207
 46 CCATGAATTAACCTCGTTAAAAAATA 21

RESULT 11
 AW967131/c
 LOCUS
 DEFINITION EST379205 MAGE resequences, MAGJ Homo sapiens cDNA, mRNA sequence.
 ACCESSION AW967131
 VERSION AW967131.1 GI:8156967
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 646)
 AUTHORS Hegde,P., Qi,R., Abernathy,K., Dharap,S., Gaspard,R., Gay,C., Holt,I.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and Quackenbush,J.
 TITLE Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray
 JOURNAL Unpublished (2000)
 COMMENT Contact: John Quackenbush
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 3528
 Fax: 301 838 0208
 Email: johnq@tigr.org
 Plate: 237
 Seq primer: Reverse.
 Location/Qualifiers
 1..646
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone_lib="MAGE resequences, MAGJ"
 /note="Vector: pBluescriptSKm"

ORIGIN
 Query Match 12.9%; Score 129.2; DB 1; Length 646;
 Best Local Similarity 84.7%; Pred. No. 3.1e-18;
 Matches 161; Conservative 0; Mismatches 18; Indels 11; Gaps 1;
 2 GCTGGGATTACAGCACCACCGCCACCATGCCAGCTAATTTTGTATTTTAGTAGAGAC 61
 549 GTTAGAATTACAGTGTCCGCCACCGCCAGCTAATTTTGTATTTTAGTAGAGAC 490
 62 GGGGGTGGGGTGGGGTTACCATGTTGGCCAGGCTGGTCTCGAAGTCTTGACCTCAGAT 121
 489 G-----GGTTTCACCATTTGACCATGTTGACCATGTTGCTCAACACCTGACCTCAGAT 441
 122 GATCCACCTGCTGCTCTCTTAAGTCTGGGATTACAGTGTGAGCCACCATGCCCGAG 181
 440 GATCCACCGCTCAGGCTCCCAAGTCTGGGATTACAGTGTGAGCCACCATGCCCGAG 381
 182 CTCAGAAATTT 191
 380 CCCAGAAATAT 371

RESULT 12
 AV693536
 LOCUS
 DEFINITION AV693536 GKC Homo sapiens cDNA clone GKCOF10 5', mRNA sequence.
 ACCESSION AV693536
 VERSION AV693536.1 GI:10295399
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 416)
 AUTHORS Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X., Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W., Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X., Hu,G., Gu,J., Chen,Z. and Han,Z.
 TITLE Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
 PUBMED 11752456
 COMMENT Contact: Zeguang Han
 Chinese National Human Genome Center at Shanghai
 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China

Tel: 86-21-50801919 (ex.45)
 Fax: 86-21-50801922
 Email: hanzg@chgc.sh.cn
 This clone is available at CHGC in Shanghai.

FEATURES

Location/Qualifiers
 1. .416
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="GKCCP10"
 /tissue_type="hepatocellular carcinoma"
 /dev_stage="Adult"
 /lab_host="SOLR"
 /clone_lib="GKC"
 /note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2: XhoI"

ORIGIN

Query Match 12.9%; Score 129; DB 1; Length 416;
 Best Local Similarity 70.2%; Pred. No. 3.5e-18;
 Matches 193; Conservative 0; Mismatches 70; Indels 12; Gaps 1;
 Qy 2 GCTGGATTACAGGACCCGCCACATGTCAGTAAATTTTGTATTTTGTATTTAGTAGAGAC 61
 Db 133 GCTGGGTTACAAGTACGACCAATGCGCGGCTAAATTTTGTATTTTGTATTTTGTATTTAGTAGAGAC 192
 Qy 62 GGGGGTGGGGTGGGGTTCACATGTTGGCCAGGCTGCTCGAACTTCTGACCTCAGAT 121
 Db 193 AGGT-----TTACCATGTTGGCCAGGCTGCTCGAACTTCTGACCTCAGGT 240
 Qy 122 GATCACCTGCTCTGCTCTCTAAAGTCTGGGATTACAGTGTGAGCCACCATGCCCGAC 181
 Db 241 GATCACCCGCTCAGCTCTCCAAAGTCTGGGATTACAGGAGGAGCCACCGCCCGAC 300
 Qy 182 CTCAGAAATTTACTCTGTTTGAACAATCTGGGCTGAGGTAGGAGCTCACCCCACTCAA 241
 Db 301 CCTAAACATTTTATCTTACCAAGAAATTCCTCAAGAGCCCTTGGTGTGCTGCCAATGCAA 360
 Qy 242 GTGTTGGTGTGTTTAAAGCAATGATAGAAATTTT 276
 Db 361 ATGTGTCACATTTTATAAGAGGGAGTTTATATTT 395

RESULT 13
 AV691556 421 bp mRNA linear EST 16-JAN-2002
 LOCUS AV691556 GKC Homo sapiens cDNA clone GKCCP11 5', mRNA sequence.
 DEFINITION AV691556
 ACCESSION AV691556.1 GI:10293419
 VERSION EST.
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo.

REFERENCE
 AUTHORS Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X.,
 Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W.,
 Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X.,
 Hu,G., Gu,J., Chen,Z. and Han,Z.
 TITLE Insight into hepatocellular carcinogenesis at transcriptome level
 by comparing gene expression profiles of hepatocellular carcinoma
 with those of corresponding noncancerous liver

JOURNAL
 PUBLISHED Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
 COMMENT 11752456
 Contact: Zeguang Han
 Chinese National Human Genome Center at Shanghai
 351 Guo Shoujing Road, Zhongjiang Hi-Tech Park, Pudong, Shanghai
 201203, P. R. China
 Tel: 86-21-50801919 (ex.45)
 Fax: 86-21-50801922
 Email: hanzg@chgc.sh.cn
 This clone is available at CHGC in Shanghai.

FEATURES

Location/Qualifiers
 1. .421
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="GKCCP11"
 /tissue_type="hepatocellular carcinoma"
 /dev_stage="Adult"
 /lab_host="SOLR"
 /clone_lib="GKC"
 /note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2: XhoI"

ORIGIN

Query Match 12.9%; Score 129; DB 1; Length 421;
 Best Local Similarity 70.2%; Pred. No. 3.5e-18;
 Matches 193; Conservative 0; Mismatches 70; Indels 12; Gaps 1;
 Qy 2 GCTGGATTACAGGACCCGCCACATGTCAGTAAATTTTGTATTTTGTATTTAGTAGAGAC 61
 Db 133 GCTGGGTTACAAGTACGACCAATGCGCGGCTAAATTTTGTATTTTGTATTTTGTATTTAGTAGAGAC 192
 Qy 62 GGGGGTGGGGTGGGGTTCACATGTTGGCCAGGCTGCTCGAACTTCTGACCTCAGAT 121
 Db 193 AGGT-----TTACCATGTTGGCCAGGCTGCTCGAACTTCTGACCTCAGGT 240
 Qy 122 GATCACCTGCTCTGCTCTCTAAAGTCTGGGATTACAGTGTGAGCCACCATGCCCGAC 181
 Db 241 GATCACCCGCTCAGCTCTCCAAAGTCTGGGATTACAGGAGGAGCCACCGCCCGAC 300
 Qy 182 CTCAGAAATTTACTCTGTTTGAACAATCTGGGCTGAGGTAGGAGCTCACCCCACTCAA 241
 Db 301 CCTAAACATTTTATCTTACCAAGAAATTCCTCAAGAGCCCTTGGTGTGCTGCCAATGCAA 360
 Qy 242 GTGTTGGTGTGTTTAAAGCAATGATAGAAATTTT 276
 Db 361 ATGTGTCACATTTTATAAGAGGGAGTTTATATTT 395

RESULT 14

AA720582 488 bp mRNA linear EST 22-JAN-1998
 LOCUS AA720582
 DEFINITION nw21h01.81 NCI CGAP GCB0 Homo sapiens cDNA clone IMAGE:1241137 3',
 similar to contains Alu repetitive element;; mRNA sequence.

ACCESSION AA720582
 VERSION AA720582.1 GI:2736717
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo.
 REFERENCE
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
 Ph.D., Gerald Marti, M.D.
 cDNA Library Preparation: Louis M. Staudt, M.D., Ph.D.
 cDNA Sequencing by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 www-bio.llnl.gov/bbrp/image/image.html
 Insert Length: 687 Std Error: 0.00
 Seq primer: -40ml3 fwd. ET from Amersham
 High quality sequence stop: 481.
 Location/Qualifiers
 1. .488
 /organism="Homo sapiens"

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/molecule="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1241137"
/tissue_type="germinal center B-cells"
/lab_host="SOLR (kanamycin resistant)"
/clone_lib="NCI CGAP GCB0"
/notes="Organ: tonsil; Vector: Bluescript SK-; Site 1:
EcORI; Site 2: XhoI; Cloned unidirectionally. Primer:
Oligo dt. Germinal center B-cells Library constructed by
Dr. L. Staudt (NCI). 5' adaptor sequence: 5'
GAATTCGGACACGAG 3' 3' adaptor sequence: 5'
CTCGAGTTTTTTTTTTTTTTT 3' Average insert size: 1.1 kb."

ORIGIN
Query Match      12.9%; Score 128.8; DB 1; Length 488;
Best Local Similarity 81.4%; Pred. No. 3.9e-18;
Matches 166; Conservative 0; Mismatches 27; Indels 11; Gaps 1;

QY 2 GCTGGGATTACAGCACCCGCCACCATGCCAGCTAATTTTTTTTGTATTTTAGTAGAGAC 61
Db 221 GCTGGGATTACAGCACCCGCCACCAAGCTGGCTAATTTTTTTGTATTTTAGTAGAGAC 280
QY 62 GGGGGTGGGGGTGGGGTTTCCACCATGTTGGCCAGGCTGGTCTCGAACTTCTGACCTCAGAT 121
Db 281 -----AGGGTTTCCACCATGTTGGCCAGGCTGGTCTCAAACTCCTGACCTCAGGT 329
QY 122 GATCCACCTGCTCTGCTCTTAAAGTGTGGGATTACAGGTGTGAGCCACCATGCCCAG 181
Db 330 GATCCACCTGCTCTGCTCTTAAAGTGTGGGATTACAGGTGTGAGCCAGCGTGGCCAG 389
QY 182 CTCAGATTACTCTGTTAGAA 205
Db 390 CCCACCATGAATTTTAAATCAA 413

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RESULT 15
BQ230374
LOCUS BQ230374 503 bp mRNA linear EST 02-MAY-2002
DEFINITION AGENCOURT_7560272 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6048631
5', mRNA sequence.
ACCESSION BQ230374
VERSION BQ230374.1 GI:20411774
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
1 (bases 1 to 603)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapba@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTMP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHAM3297 row: p column: 08
High quality sequence stop: 602.
Location/Qualifiers
1 .603
/organism="Homo sapiens"
/molecule="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6048631"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_72"
/note="Organ: sKin; Vector: pCMV-SPORT6; Site_1: NotI;

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Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 2 kb. Library constructed by Life
Technologies."

ORIGIN
Query Match      12.9%; Score 128.8; DB 3; Length 603;
Best Local Similarity 85.1%; Pred. No. 3.8e-18;
Matches 160; Conservative 0; Mismatches 17; Indels 11; Gaps 1;

QY 2 GCTGGGATTACAGGCACCCGCCACCATGCCAGCTAATTTTTTTGTATTTTAGTAGAGAC 61
Db 142 GCTGGGATTACAGGCACCCGCCACCATGCCAGCTAATTTTTTTGTATTTTAGTAGAGAC 201
QY 62 GGGGGTGGGGGTGGGGTTTCCACCATGTTGGCCAGGCTGGTCTCGAACTTCTGACCTCAGAT 121
Db 202 G-----GGGTTTGGCCATGTTGGCCAGGCTGGTCTCGAACTTCTGACCTCAGGT 250
QY 122 GATCCACCTGCTCTGCTCTTAAAGTGTGGGATTACAGGTGTGAGCCACCATGCCCAG 181
Db 251 GATCCACCTGCTCTGCTCTTAAAGTGTGGGATTACAGGTGTGAGCCACCATGCTCAG 310
QY 182 CTCAGAAAT 189
Db 311 CCTGAAT 318

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Search completed: January 10, 2006, 15:07:46
Job time : 4715 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 10, 2006, 10:27:39 ; Search time 205 Seconds
(without alignments)
8679.704 Million cell updates/sec

Title: US-09-615-039-1_COPY_11500_12500

Perfect score: 1001

Sequence: 1 ggtgggattacaggcacc.....gggaccagtggcgtgtggc 1001

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2_6/ptodata/1/ina/1 COMB.seq.*
- 2: /cgn2_6/ptodata/1/ina/5 COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/H COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/PTCUS COMB.seq.*
- 7: /cgn2_6/ptodata/1/ina/PP COMB.seq.*
- 8: /cgn2_6/ptodata/1/ina/RE COMB.seq.*
- 9: /cgn2_6/ptodata/1/ina/backfiles.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1001	100.0	4321	3	US-09-402-181B-6
2	1001	100.0	15418	3	US-09-783-203-1
3	1001	100.0	15418	3	US-09-994-427A-1
4	1001	100.0	15418	3	US-09-244-438-1
5	1001	100.0	15418	3	US-09-995-419A-1
6	1001	100.0	44952	3	US-09-949-016-12197
7	1001	100.0	44960	3	US-09-949-016-17583
8	972.8	97.2	51552	3	US-09-733-294A-30
9	930.8	93.0	4335	3	US-08-974-549A-6
10	930.8	93.0	4335	3	US-09-721-456-6
11	677.8	67.7	35871	3	US-09-956-335-2
12	677.8	67.7	35978	3	US-09-956-335-1
13	676	67.5	1677	3	US-09-956-335-3
14	497	49.7	497	3	US-09-244-438-22
15	229.8	23.0	4200	3	US-08-912-931-6
16	134.2	13.4	18596	3	US-09-318-448-11
17	134.2	13.4	18596	3	US-09-577-266-11
18	134.2	13.4	18597	3	US-09-962-665-8
19	134.2	13.4	18597	3	US-09-963-333-8
20	134.2	13.4	18597	3	US-09-962-677-8
21	134.2	13.4	19383	3	US-09-949-016-16031
22	134.2	13.4	45716	3	US-08-965-048-5
23	134.2	13.4	45989	3	US-08-965-048-6
24	132.4	13.2	108060	3	US-09-949-016-13159

25	132.4	13.2	121234	3	US-09-949-016-14142	Sequence 14142, A
26	132.4	13.2	140315	3	US-09-949-016-14141	Sequence 14141, A
c 27	132.2	13.2	26760	3	US-09-949-016-15894	Sequence 15894, A
28	131.8	13.2	3129	3	US-10-045-428A-9	Sequence 9, Appli
29	131.8	13.2	137949	3	US-09-949-016-12196	Sequence 12196, A
30	131.8	13.2	137956	3	US-09-949-016-17260	Sequence 17260, A
31	131.6	13.1	601	3	US-09-949-016-162869	Sequence 162869, A
32	131.6	13.1	140925	3	US-09-949-016-11777	Sequence 11777, A
33	131.6	13.1	140982	3	US-09-949-016-66371	Sequence 66371, A
34	131.4	13.1	601	3	US-09-949-016-66371	Sequence 66371, A
c 35	131.2	13.1	60304	3	US-09-949-016-12218	Sequence 12218, A
c 36	131.2	13.1	60305	3	US-09-949-016-15791	Sequence 15791, A
37	131	13.1	121982	3	US-09-949-016-12085	Sequence 12085, A
38	131	13.1	121982	3	US-09-949-016-14105	Sequence 14105, A
39	130.2	13.0	91831	3	US-09-949-016-13694	Sequence 13694, A
40	129.8	13.0	601	3	US-09-949-016-66372	Sequence 66372, A
c 41	129.8	13.0	129554	3	US-09-949-002-765	Sequence 765, App
42	129.8	13.0	246230	3	US-09-949-016-17019	Sequence 17019, A
c 43	129.8	13.0	246230	3	US-09-949-016-17019	Sequence 17019, A
44	129.8	13.0	246230	3	US-09-949-016-17020	Sequence 17020, A
c 45	129.8	13.0	246230	3	US-09-949-016-17020	Sequence 17020, A

ALIGNMENTS

RESULT 1

US-09-402-181B-6
; Sequence 6, Application US/09402181B
; Patent No. 6610839
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 633
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09402,181B
; FILING DATE: 29-Sep-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997


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; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ausenhus, Scott L.
; REGISTRATION NUMBER: 42,271
; REFERENCE/DOCKET NUMBER: 015389-002620US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4321 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..4321
; OTHER INFORMATION: /note= "genomic DNA insert of pGRN144"
; FEATURE:
; NAME/KEY: intron
; LOCATION: 2702..2804
; OTHER INFORMATION: /note= "intron 1"
; FEATURE:
; NAME/KEY: intron
; LOCATION: 4160..4313
; OTHER INFORMATION: /note= "intron 2"
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-402-181B-6

Query Match
Best Local Similarity 100.0%; Score 1001; DB 3; Length 4321;
Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGCTGGGATTACAGGACCGCCACCATGCCAGCTAAATTTTGTATTTTGTAGTAGAGA 60
Db 438 GGCTGGGATTACAGGACCGCCACCATGCCAGCTAAATTTTGTATTTTGTAGTAGAGA 497

Qy 61 CGGGGGTGGGGGTGGGGTTCACCATGTTGGCCAGGCTGGTCTCGAACTTCTGACCTCAGA 120
Db 498 CGGGGGTGGGGGTGGGGTTCACCATGTTGGCCAGGCTGGTCTCGAACTTCTGACCTCAGA 557

Qy 121 TGATCCACCTGCTCTGCTCTCTAAAGTGTGGGATTACAGGTTGAGCCACCATGCCCA 180
Db 558 TGATCCACCTGCTCTGCTCTCTAAAGTGTGGGATTACAGGTTGAGCCACCATGCCCA 617

Qy 181 GCTCAGAAATTACTCTGTTTAGAACATCTGGGTCTGAGGTAGGAAGCTCACCCCACTCA 240
Db 618 GCTCAGAAATTACTCTGTTTAGAACATCTGGGTCTGAGGTAGGAAGCTCACCCCACTCA 677

Qy 241 AGTGTGTGGTGTGTTTAAAGCAATGATAGAAATTTTATTTTGTGTTAGAACACTCTTGA 300
Db 678 AGTGTGTGGTGTGTTTAAAGCAATGATAGAAATTTTATTTTGTGTTAGAACACTCTTGA 737

Qy 301 TGTTTTACATGTGATGACATAAGACATCATCAGCTTTTCAAAGACACACTAACTGCACCC 360
Db 738 TGTTTTACATGTGATGACATAAGACATCATCAGCTTTTCAAAGACACACTAACTGCACCC 797

Qy 361 ATAATATCGGGTGTCTTCTGGGTATCAGCGATCTTCATTTCAATGTCGGGAGGGGTTTCC 420
Db 798 ATAATATCGGGTGTCTTCTGGGTATCAGCGATCTTCATTTCAATGTCGGGAGGGGTTTCC 857

Qy 421 TCGGCATGCACATGGTGTGTTAACTACTCAGCATATCTTCTGCTTCCATTTCTTCTTTC 480
Db 858 TCGGCATGCACATGGTGTGTTAACTACTCAGCATATCTTCTGCTTCCATTTCTTCTTTC 917

Qy 481 CCTCTTTTAAATTTGTTTCTAATGTTGGTTCTCTGCGAGAGAACCAAGTGAAGTACA 540
Db 918 CCTCTTTTAAATTTGTTTCTAATGTTGGTTCTCTGCGAGAGAACCAAGTGAAGTACA 977

Qy 541 ACTTAACTTTTGTGGAAACAAATTTTCCAAACCGCCCTTTGCCCTAGTGGCAGAGACAA 600

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Db 1038 TTCACAAACACAGCCCTTTAAAAAGGCTTAGGGATCACTAAGGGGATTTCTAGAAGAGCG 1097
Qy 661 ACCGTAATCTTAAGTATTACAAAGCAGGCTTAACTCCAGCGAGGTCACAGCCCGAGG 720
Db 1098 ACCGTAATCTTAAGTATTACAAAGCAGGCTTAACTCCAGCGAGGTCACAGCCCGAGG 1157
Qy 721 GAGGGTCGAGGCTGTTCAAAATGCTAGCTTCATAATAAAGCAATTTCTCCGGCAGTT 780
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Qy 781 TCTGAAAGTAGGAAAGGTTACATTTAAAGGTTGCTTTGTAGCAATTTCACTGTTTGCCTGA 840
Db 1218 TCTGAAAGTAGGAAAGGTTACATTTAAAGGTTGCTTTGTAGCAATTTCACTGTTTGCCTGA 1277
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Db 1278 CCTCAGCTACAGCATCCCTGCAAGGCTCGGGAGACCCAGAGTTTCTCGCCCTTAGAT 1337
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Db 1338 CCAAACTTGAGCAACCGGAGTCTGATTCTCGGGAAGTCTCAGCTGTCTCGGGTGTG 1397
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Db 1398 GCCGGGGCCCCAGGTCCTGGAGGGGACCAAGTGGCCGCTGTGGC 1438

RESULT 2
US-09-783-203-1
; Sequence 1, Application US/09783203
; Patent No. 6576464
; GENERAL INFORMATION:
; APPLICANT: Genon Corporation
; APPLICANT: Gold, Joseph
; APPLICANT: Lebkowski, Jane
; TITLE OF INVENTION: Tpacked stem cells
; FILE REFERENCE: 096/003
; CURRENT APPLICATION NUMBER: US/09/783,203
; CURRENT FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: 60/253,443
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/253,357
; PRIOR FILING DATE: 2000-11-27
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 1
; LENGTH: 15418
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-783-203-1

Query Match
Best Local Similarity 100.0%; Score 1001; DB 3; Length 15418;
Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGCTGGGATTACAGGACCGCCACCATGCCAGCTAAATTTTGTATTTTGTAGTAGAGA 60
Db 11500 GGCTGGGATTACAGGACCGCCACCATGCCAGCTAAATTTTGTATTTTGTAGTAGAGA 11559

Qy 61 CGGGGGTGGGGGTGGGGTTCACCATGTTGGCCAGGCTGGTCTCGAACTTCTGACCTCAGA 120
Db 11560 CGGGGGTGGGGGTGGGGTTCACCATGTTGGCCAGGCTGGTCTCGAACTTCTGACCTCAGA 11619

Qy 121 TGATCCACCTGCTCTGCTCTCTAAAGTGTGGGATTACAGGTTGAGCCACCATGCCCA 180
Db 11620 TGATCCACCTGCTCTGCTCTCTAAAGTGTGGGATTACAGGTTGAGCCACCATGCCCA 11679

Qy 181 GCTCAGAAATTACTCTGTTTAGAACATCTGGGTCTGAGGTAGGAAGCTCACCCCACTCA 240

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Db 11680 GCTCAGAAATTTACTCTCTGTTTAAAGCAATCTGGGTCTGAGGTAGGAAGCTCACCCCACTCA 11739
Qy 241 AGTGTCTGGTGTGTTTAAAGCAATGATAGAAATTTTATTTGTTGTTAGAACACTCTTGA 300
Db 11740 AGTGTCTGGTGTGTTTAAAGCAATGATAGAAATTTTATTTGTTGTTAGAACACTCTTGA 11799
Qy 301 TGTTTTACACTGTGATGACTAAGACATCATCAGCTTTTCAAAGACACACTAACTGCAACC 360
Db 11800 TGTTTTACACTGTGATGACTAAGACATCATCAGCTTTTCAAAGACACACTAACTGCAACC 11859
Qy 361 ATAATACCTGGGGTCTCTTGGGTATCAGCATCTTCAATGAAATGCGGGAGGGTTC 420
Db 11860 ATAATACCTGGGGTCTCTTGGGTATCAGCATCTTCAATGAAATGCGGGAGGGTTC 11919
Qy 421 TCGCCATGCAATGTTTAAATTAATCTCCAGCATATCTTCTGCTTCCATTTCTCTCTTC 480
Db 11920 TCGCCATGCAATGTTTAAATTAATCTCCAGCATATCTTCTGCTTCCATTTCTCTCTTC 11979
Qy 481 CCTCTTTTAAATTTGTTTCTATGTTGGCTTCTCTGAGAGAACAGTGTAAAGTACA 540
Db 11980 CCTCTTTTAAATTTGTTTCTATGTTGGCTTCTCTGAGAGAACAGTGTAAAGTACA 12039
Qy 541 ACTTAACTTTTGTGGAACAAATTTTCAAACCGCCCTTTGCCCTAGTGCAGACAA 600
Db 12040 ACTTAACTTTTGTGGAACAAATTTTCAAACCGCCCTTTGCCCTAGTGCAGACAA 12099
Qy 601 TTCAAAACACAGCCCTTTAAAGGCTTAGGGATCACTAAGGGATTTCTAGAGAGCG 660
Db 12100 TTCAAAACACAGCCCTTTAAAGGCTTAGGGATCACTAAGGGATTTCTAGAGAGCG 12159
Qy 661 ACCGTAACTCTAAGTATTTAAAGAGGCTTAGGGATCACTAAGGGATTTCTAGAGAGCG 720
Db 12160 ACCGTAACTCTAAGTATTTAAAGAGGCTTAGGGATCACTAAGGGATTTCTAGAGAGCG 12219
Qy 721 GAGGTGCGAGCCCTGTTCAAATGCTAGCTCCATAAATAAAGCAATTTCTCCGCGAGTT 780
Db 12220 GAGGTGCGAGCCCTGTTCAAATGCTAGCTCCATAAATAAAGCAATTTCTCCGCGAGTT 12279
Qy 781 TCTGAAAGTAGGAAGGTTTCAATTAAGGTTGCGTTTGTAGCAATTTCAAGTGTTCGCA 840
Db 12280 TCTGAAAGTAGGAAGGTTTCAATTAAGGTTGCGTTTGTAGCAATTTCAAGTGTTCGCA 12339
Qy 841 CCTCAGCTACAGCATCCCTGCAAGCCCTCGGAGACCCAGAAATTTCTCGCCCTTAGAT 900
Db 12340 CCTCAGCTACAGCATCCCTGCAAGCCCTCGGAGACCCAGAAATTTCTCGCCCTTAGAT 12399
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Db 12400 CCAAACTTGAGCAACCGGAGTCTGGATTCTCGGGAAGTCTCTCAGCTGCTCGCGGTTGT 12459
Qy 961 GCCGGGGCCCGAGTCTGGAGGGACAGTGGCCGTGTGGC 1001
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RESULT 3

US-09-994-427A-1
; Sequence 1, Application US/09994427A
; Patent No. 6713055
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Schliff, J. Michael
; TITLE OF INVENTION: GLYCOSYLTRANSFERASE VECTORS FOR TREATING CANCER
; FILE REFERENCE: 083,002
; CURRENT APPLICATION NUMBER: US/09/994,427A
; CURRENT FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: 60/253,395
; PRIOR FILING DATE: 2000-11-27
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 15418
; TYPE: DNA

; ORGANISM: Homo sapiens
US-09-994-427A-1
Query Match 100.0%; Score 1001; DB 3; Length 15418;
Best Local Similarity 100.0%; Pred. No. 2.1e-287; Indels 0; Gaps 0;
Matches 1001; Conservative 0; Mismatches 0
Qy 1 GGCCTGGGATTTACAGGCAACCGCCCAACATGCCCAGCTAAATTTTGTATTTTGTAGTACAGA 60
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Db 11800 TGTTTTACACTGTGATGACTAAGCAATCATCAGCTTTTCAAAGACACACTAACTGCAACC 11859
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Db 11860 ATAATACCTGGGGTCTCTTGGGTATCAGCATCTTCAATGAAATGCGGGAGGGTTC 11919
Qy 421 TCGCCATGCAATGTTTAAATTAATCTCCAGCATATCTTCTGCTTCCATTTCTCTCTTC 480
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Qy 481 CCTCTTTTAAATTTGTTTCTATGTTGGCTTCTCTGAGAGAACAGTGTAAAGTACA 540
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Db 12040 ACTTAACTTTTGTGGAACAAATTTTCAAACCGCCCTTTGCCCTAGTGCAGACAA 12099
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Db 12280 TCTGAAAGTAGGAAGGTTTCAATTAAGGTTGCGTTTGTAGCAATTTCAAGTGTTCGCGA 12339
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RESULT 4
US-09-244-438-1
; Sequence 1, Application US/09244438
; Patent No. 6777203
; GENERAL INFORMATION:
; APPLICANT: Morin, Gregg B.
; APPLICANT: Lichtsteiner, Serge
; APPLICANT: Vasserot, Alain
; APPLICANT: Adams, Robert R.
; APPLICANT: Geron Corporation
; TITLE OF INVENTION: Telomerase Reverse Transcriptase Transcriptional
; FILE OF INVENTION: Regulatory Sequences and Methods of Using
; FILE REFERENCE: 019/246P
; CURRENT APPLICATION NUMBER: US/09/244,438
; CURRENT FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 15418
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Human TERT promoter
US-09-244-438-1

Query Match 100.0%; Score 1001; DB 3; Length 15418;
Best Local Similarity 100.0%; Pred. No. 2.1e-287;
Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 121 TGATCCACCTGCTCTGCCCTCTAAAGTGTGGGATTTACAGGTGTGAGCCACCATGCCCA 180
Db 11620 TGATCCACCTGCTCTGCCCTCTAAAGTGTGGGATTTACAGGTGTGAGCCACCATGCCCA 11679
Qy 181 GCTCAGAAATTTACTCTGTTTAGAAACATCTGGGFTCAGGTGAGGAAGCTCACCCCACTCA 240
Db 11680 GCTCAGAAATTTACTCTGTTTAGAAACATCTGGGFTCAGGTGAGGAAGCTCACCCCACTCA 11739
Qy 241 AGTGTGTGTGTGTTTAAAGCCAAATGATAGAAATTTTATTTTGTAGAACACTCTTGA 300
Db 11740 AGTGTGTGTGTGTTTAAAGCCAAATGATAGAAATTTTATTTTGTAGAACACTCTTGA 11799
Qy 301 TGTTTTACCTGTGATGACTAAGACATCATCAGCTTTTCAAAGACACACTAAGTGCACCC 360
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Qy 421 TCGCCATGCACATGCTGTTAATTAATCTCCAGCATAACTCTGCTTCCATTTCTTCTCTTC 480
Db 11920 TCGCCATGCACATGCTGTTAATTAATCTCCAGCATAACTCTGCTTCCATTTCTTCTCTTC 11979
Qy 481 CCTCTTTTAAATTTGTGTTTCTATGTTGGCTTCTCTGCAGAGAACCAAGTGAAGTACCA 540
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Db 12100 TTCAAAAACACAGCCCTTTTAAAGGGCTTAGGGATCACTAAGGGGATTTCTAGNAGAGCG 12159
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Db 12160 ACCCGTAATCTTAAGTATTTTACAAGACGAGGCTTAACCTTCAGCGAGCGTGCACAGCCAGG 12219
Qy 721 GAGGTGCGAGGGCTGTTCAAATGCTAGCTTCAATAATAAGCAATTTCTCCGGGAGTTT 780
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Qy 841 CCTCAGCTACAGCATCTCCGCAAGGCTCGGGAGACCCAGAAAGTTTCTCCGCCCTTAGAT 900
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Qy 901 CCAAACTTGAGCAACCGGAGTCTGGATTTCTTGGGAGTCTCAGCTGTCTCGGGTGT 960
Db 12400 CCAAACTTGAGCAACCGGAGTCTGGATTTCTTGGGAGTCTCAGCTGTCTCGGGTGT 12459
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RESULT 5
US-09-995-419A-1
; Sequence 1, Application US/09995419A
; Patent No. 6921665
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: McWhir, Jim
; APPLICANT: Gold, Joseph D.
; APPLICANT: Schiff, J. Michael
; TITLE OF INVENTION: 096,004 - SeqList
; FILE REFERENCE: 096,004 - SeqList
; CURRENT APPLICATION NUMBER: US/09/995,419A
; PRIOR FILING DATE: 2001-11-26
; PRIOR FILING DATE: 2000-11-27
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 15418
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-995-419A-1

Query Match 100.0%; Score 1001; DB 3; Length 15418;
Best Local Similarity 100.0%; Pred. No. 2.1e-287;
Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCGTGGGATTTACAGGACCCCGCCACCATGCGCCAGTAAATTTTGTATTTTGTAGTAGAGA 60
Db 11500 GCGTGGGATTTACAGGACCCCGCCACCATGCGCCAGTAAATTTTGTATTTTGTAGTAGAGA 11559
Qy 61 CGGGGGTGGGGTGGGGTTCACCATGTTGGCCAGGGCTGGTCTCGAACTTCTGACCTCAGA 120
Db 11560 CGGGGGTGGGGTGGGGTTCACCATGTTGGCCAGGGCTGGTCTCGAACTTCTGACCTCAGA 11619
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Db 11620 TGATCCACCTGCTCTGCCCTCTAAAGTGTGGGATTTACAGGTGTGAGCCACCATGCCCA 11679
Qy 181 GCTCAGAAATTTACTCTGTTTAGAAACATCTGGGFTCAGGTGAGGAAGCTCACCCCACTCA 240
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Qy 301 TGTTTTACCTGTGATGACTAAGACATCATCAGCTTTTCAAAGACACACTAAGTGCACCC 360
Db 11800 TGTTTTACCTGTGATGACTAAGACATCATCAGCTTTTCAAAGACACACTAAGTGCACCC 11859
Qy 361 ATAATACCTGGGGTGTCTTCTGGGTATCAGGATCTTCAATGAATCCGGGAGGGGTTTCC 420
Db 11860 ATAATACCTGGGGTGTCTTCTGGGTATCAGGATCTTCAATGAATCCGGGAGGGGTTTCC 11919
Qy 421 TCGCCATGCACATGCTGTTAATTAATCTCCAGCATAACTCTGCTTCCATTTCTTCTCTTC 480
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Qy 481 CCTCTTTTAAATTTGTGTTTCTATGTTGGCTTCTCTGCAGAGAACCAAGTGAAGTACCA 540
Db 11980 CCTCTTTTAAATTTGTGTTTCTATGTTGGCTTCTCTGCAGAGAACCAAGTGAAGTACCA 12039
Qy 541 ACTTAACCTTTTGTGGAAACAAATTTTCAAACCGCCCTTTGCCCTAGTGGCAGAGACAA 600
Db 12040 ACTTAACCTTTTGTGGAAACAAATTTTCAAACCGCCCTTTGCCCTAGTGGCAGAGACAA 12099
Qy 601 TTCAACAACACAGCCCTTTTAAAGGGCTTAGGGATCACTAAGGGGATTTCTTAGAAGAGCG 660
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Db 911 CCAAACCTTGAGCAACCGGAGTCTGGATTCCTGGGAAGTCTCAGCTGTCTCGGTTGT 970
Qy 961 GCGGGGCCCGCAGTCTGGAGGGACCAAGTGGCGTGTGGC 1001
Db 971 GCGGGGCCCGCAGTCTGGAGGGACCAAGTGGCGTGTGGC 1011

RESULT 7
US-09-949-016-17583
; Sequence 17583, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CU001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17583
; LENGTH: 44960
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(44960)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17583

Query Match 100.0%; Score 1001; DB 3; Length 44960;
Best Local Similarity 100.0%; Pred. No. 3.5e-287;
Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGCTGGGATTACAGGCACCCGCCACCATGCCAGCTAAATTTTGTATTTTGTAGTAGA 60
Db 11 GGCTGGGATTACAGGCACCCGCCACCATGCCAGCTAAATTTTGTATTTTGTAGTAGA 70

Qy 61 CGGGGGTGGGGTGGGGTTCACCATGTGGCCAGCTGGTCTCGAATCTTGACCTCAGA 120
Db 71 CGGGGGTGGGGTGGGGTTCACCATGTGGCCAGCTGGTCTCGAATCTTGACCTCAGA 130

Qy 121 TGATCCACCTGCCTCTGCCTCTAAAGTCTGGGATTACAGGTGTGAGCCACCATGCCCA 180
Db 131 TGATCCACCTGCCTCTGCCTCTAAAGTCTGGGATTACAGGTGTGAGCCACCATGCCCA 190

Qy 181 GCTCAGAAATTTACTCTGTTTGAAGAACATCTGGGTCTGAGGTAGGAAGCTCACCCACTCA 240
Db 191 GCTCAGAAATTTACTCTGTTTGAAGAACATCTGGGTCTGAGGTAGGAAGCTCACCCACTCA 250

Qy 241 AGTGTGTGGTGTGTTTAAAGCAATGATAGAAATTTTATTTTGTAGTAACTCTTGA 300
Db 251 AGTGTGTGGTGTGTTTAAAGCAATGATAGAAATTTTATTTTGTAGTAACTCTTGA 310

Qy 301 TGTTTTACATGTCATCAAGACATCATCAGCTTTTCAAAGACACACTAACTGACACC 360
Db 311 TGTTTTACATGTCATCAAGACATCATCAGCTTTTCAAAGACACACTAACTGACACC 370

Qy 361 ATAATCTGGGGTGTCTTCTGGGTATCAGGATCTTCATTGAATCGCGGAGGGTTC 420
Db 371 ATAATCTGGGGTGTCTTCTGGGTATCAGGATCTTCATTGAATCGCGGAGGGTTC 430

Qy 421 TCGCATGCATGGTGTAAATTAATCTCAGCAATCTTCTGCTTCAATTTCTCTTC 480
Db 431 TCGCATGCATGGTGTAAATTAATCTCAGCAATCTTCTGCTTCAATTTCTCTTC 490

Qy 481 CCTCTTTTAAATTTGTTTCTATGTTGGCTTCTCTGCAGAGAACCAAGTGAAGCTACA 540

Db 491 CCTCTTTTAAATTTGTTTCTATGTTGCTTCTCTGCAGAGAACCCAGTGAAGCTACA 550
Qy 541 ACTTAACCTTTTGTGGAAACAAATTTTCCAAACCGCCCTTTGCCCTAGTGGCAGACAA 600
Db 551 ACTTAACCTTTTGTGGAAACAAATTTTCCAAACCGCCCTTTGCCCTAGTGGCAGACAA 610

Qy 601 TTCACAAACACACGCGCTTTTAAAGGCTTAGGGATCACTAAAGGGGATTTCTAGAAAGCG 660
Db 611 TTCACAAACACACGCGCTTTTAAAGGCTTAGGGATCACTAAAGGGGATTTCTAGAAAGCG 670

Qy 661 ACCCGTAATCCTTAAGTATTTTACAAGACGAGGCTTAACCTCCAGCGAGCGTGACAGCCAGG 720
Db 671 ACCCGTAATCCTTAAGTATTTTACAAGACGAGGCTTAACCTCCAGCGAGCGTGACAGCCAGG 730

Qy 721 GAGGGTGGAGGCGCTGTTCAATGCTAGCTCCATTAATAAAGCAATTTCTCCGGCAGTT 780
Db 731 GAGGGTGGAGGCGCTGTTCAATGCTAGCTCCATTAATAAAGCAATTTCTCCGGCAGTT 790

Qy 781 TCTGAAAGTAGGAAGGTTACATTTAAGGTTGCTTTGTTAGCATTTTCACTGTTTCCGA 840
Db 791 TCTGAAAGTAGGAAGGTTACATTTAAGGTTGCTTTGTTAGCATTTTCACTGTTTCCGA 850

Qy 841 CCTCAGCTACAGCATCCCTGCAAGGCTCCGAGGAGACCCAGAGTTTCTCGCCCTTAGAT 900
Db 851 CCTCAGCTACAGCATCCCTGCAAGGCTCCGAGGAGACCCAGAGTTTCTCGCCCTTAGAT 910

Qy 901 CCAAACTTGAGCAACCCGAGTCTGGATTCCTGGGAGAGCCAGTGGCCGTGGC 1001
Db 911 CCAAACTTGAGCAACCCGAGTCTGGATTCCTGGGAGAGCCAGTGGCCGTGGC 970

Qy 961 GCGGGGCCCGCAGTCTGGAGGGGACCAAGTGGCCGTGGC 1001
Db 971 GCGGGGCCCGCAGTCTGGAGGGGACCAAGTGGCCGTGGC 1011

RESULT 8
US-09-733-294A-30
; Sequence 30, Application US/09733294A
; Patent No. 6492171
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: William Gaarde
; APPLICANT: Susan M. Freier
; APPLICANT: Edward V. Wanciewicz
; TITLE OF INVENTION: ANTISENSE MODULATION OF TERT EXPRESSION
; FILE REFERENCE: ISPH-0527
; CURRENT APPLICATION NUMBER: US/09/733,294A
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 09/572,423
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 108
; SEQ ID NO 30
; LENGTH: 51552
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: exon
; LOCATION: (1)...(11492)
; OTHER INFORMATION: exon 1
; NAME/KEY: intron
; LOCATION: (11493)...(11596)
; OTHER INFORMATION: intron 1
; NAME/KEY: exon
; LOCATION: (11597)...(12950)
; OTHER INFORMATION: exon 2
; NAME/KEY: intron
; LOCATION: (12951)...(21566)
; OTHER INFORMATION: intron 2
; NAME/KEY: exon
; LOCATION: (21567)...(21762)
; OTHER INFORMATION: exon 3
; NAME/KEY: intron

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; LOCATION: (21763)...(23851)
; OTHER INFORMATION: intron 3
; NAME/KEY: exon
; LOCATION: (23852)...(24032)
; OTHER INFORMATION: exon 4
; NAME/KEY: intron
; LOCATION: (24033)...(24719)
; OTHER INFORMATION: intron 4
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; LOCATION: (24720)...(24899)
; OTHER INFORMATION: exon 5
; NAME/KEY: intron
; LOCATION: (24900)...(25393)
; OTHER INFORMATION: intron 5
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; LOCATION: (25394)...(25549)
; OTHER INFORMATION: exon 6
; NAME/KEY: intron
; LOCATION: (25550)...(30196)
; OTHER INFORMATION: intron 6
; NAME/KEY: exon
; LOCATION: (30195)...(30292)
; OTHER INFORMATION: exon 7
; NAME/KEY: intron
; LOCATION: (30293)...(31272)
; OTHER INFORMATION: intron 7
; NAME/KEY: exon
; LOCATION: (31273)...(31358)
; OTHER INFORMATION: exon 8
; NAME/KEY: intron
; LOCATION: (31359)...(33843)
; OTHER INFORMATION: intron 8
; NAME/KEY: unsure
; LOCATION: 31450
; OTHER INFORMATION: unknown
; NAME/KEY: exon
; LOCATION: (33844)...(33957)
; OTHER INFORMATION: exon 9
; NAME/KEY: intron
; LOCATION: (33958)...(35941)
; OTHER INFORMATION: intron 9
; NAME/KEY: exon
; LOCATION: (35942)...(36013)
; OTHER INFORMATION: exon 10
; NAME/KEY: intron
; LOCATION: (36014)...(37884)
; OTHER INFORMATION: intron 10
; NAME/KEY: exon
; LOCATION: (37885)...(38073)
; OTHER INFORMATION: exon 11
; NAME/KEY: intron
; LOCATION: (38074)...(41874)
; OTHER INFORMATION: intron 11
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; LOCATION: (41875)...(42001)
; OTHER INFORMATION: exon 12
; NAME/KEY: intron
; LOCATION: (42002)...(42881)
; OTHER INFORMATION: intron 12
; NAME/KEY: exon
; LOCATION: (42882)...(42943)
; OTHER INFORMATION: exon 13
; NAME/KEY: intron
; LOCATION: (42944)...(46129)
; OTHER INFORMATION: intron 13
; NAME/KEY: exon
; LOCATION: (46130)...(46254)
; OTHER INFORMATION: exon 14
; NAME/KEY: intron
; LOCATION: (46255)...(47035)
; OTHER INFORMATION: intron 14
; NAME/KEY: exon
; LOCATION: (47036)...(47173)
; OTHER INFORMATION: exon 15
; LOCATION: (47174)...(47709)
; OTHER INFORMATION: intron 15
; NAME/KEY: exon
; LOCATION: (47710)...(50544)
; OTHER INFORMATION: exon 16
; US-09-733-294A-30

Query Match 97.2%; Score 972.8; DB 3; Length 51552;
Best Local Similarity 99.5%; Pred. No. 9.3e-279;
Matches 997; Conservative 0; Mismatches 2; Indels 3; Gaps 2;

Qy 1 GGCTGGGATTACAGGCACCGCCACCATGCGCCAGCTAAATTTTGTATTTTGTAGTAGAGA 60
Db 9230 GGCTGGGATTACAGGCACCGCCACCATGCGCCAGCTAAATTTTGTATTTTGTAGTAGAGA 9289

Qy 61 CGGGGTGGGGGTGGGGTTCAACATGTTGGCCAGGCTGGTCTCGAACTTCTGACCTCAGA 120
Db 9290 CGGGGT - GGGTGGGGTTCAACATGTTGGCCAGGCTGGTCTCGAACTTCTGACCTCAGA 9347

Qy 121 TGATCCACCTGCTCTGCTCTTAAGTGTGGGATTACAGGTGTGAGCCACCATGCCCA 180
Db 9348 TGATCCACCTGCTCTGCTCTTAAGTGTGGGATTACAGGTGTGAGCCACCATGCCCA 9407

Qy 181 GCTCAGAAATTTACTCTGTTTAGAAACATCTGGGTCTGAGGTAGGAAGCTCACCCCACTCA 240
Db 9408 GCTCAGAAATTTACTCTGTTTAGAAACATCTGGGTCTGAGGTAGGAAGCTCACCCCACTCA 9467

Qy 241 AGTGTGTGGTGTGTTTAAAGCCAAATGATAGAAATTTTTTATTTGTTGTAGAAACACTCTTGA 300
Db 9468 AGTGTGTGGTGTGTTTAAAGCCAAATGATAGAAATTTTTTATTTGTTGTAGAAACACTCTTGA 9527

Qy 301 TGTTTACACTGTGATGACTAAGACATCATCAGCTTTTCAAAGACACACTAACTGCACCC 360
Db 9528 TGTTTACACTGTGATGACTAAGACATCATCAGCTTTTCAAAGACACACTAACTGCACCC 9587

Qy 361 ATAATACCTGGGTGCTCTTCTGGGTATCAGCGATCTTCATTAAGTCCGGGAGGGGTTCC 420
Db 9588 ATAATACCTGGGTGCTCTTCTGGGTATCAGCGATCTTCATTAAGTCCGGGAGGGGTTCC 9647

Qy 421 TCGCCATGCACATGGTGTAAATTAATCTCCAGCATAACTCTCTGTTCATTTCTCTTC 480
Db 9648 TCGCCATGCACATGGTGTAAATTAATCTCCAGCATAACTCTCTGTTCATTTCTCTTC 9707

Qy 481 CTTCTTTTAAATTTGTGTTTCTATGTTGGTTCTCTGCAGAGAACCGAGTGTAGCTACA 540
Db 9708 CTTCTTTTAAATTTGTGTTTCTATGTTGGTTCTCTGCAGAGAACCGAGTGTAGCTACA 9767

Qy 541 ACTTAACCTTTTGTGGAAACAAATTTTCCAAACCGCCCTTTGCCCTAGTGGCAGACAA 600
Db 9768 ACTTAACCTTTTGTGGAAACAAATTTTCCAAACCGCCCTTTGCCCTAGTGGCAGACAA 9827

Qy 601 TTCACAAACACAGCCCTTTTAAAAAGGCTTAGGGATCACTAAGGGGATTTCTAGAGAGCG 660
Db 9828 TTCACAAACACAGCCCTTTTAAAAAGGCTTAGGGATCACTAAGGGGATTTCTAGAGAGCG 9887

Qy 661 ACCGTAATCTTAAGTATTTTCAAAGAGAGGCTAACTTCCAGCGAGGTGACAGCCAGG 720
Db 9888 ACCGTAATCTTAAGTATTTTCAAAGAGAGGCTAACTTCCAGCGAGGTGACAGCCAGG 9947

Qy 721 GAGGGTGGAGGCGCTGTTCAAATGCTAGCTCCATAAATAAGCAATTTCTCCGSCAGTT 780
Db 9948 GAGGGTGGAGGCGCTGTTCAAATGCTAGCTCCATAAATAAGCAATTTCTCCGSCAGTT 10007

Qy 781 TCTCAAAAGTAGGAAAGGTTTAAATTAAGGTTGCGTTTGTAGTCAATTTCAAGTGTTCGCGA 840
Db 10008 TCTCAAAAGTAGGAAAGGTTTAAATTAAGGTTGCGTTTGTAGTCAATTTCAAGTGTTCGCGA 10067

Qy 841 CCTCAGCTACAGCATCCCTGCAAGGCTTCGGGAGACCCAGAGTTTCTCG - CCCTTTAGA 899
Db 10068 CCTCAGCTACAGCATCCCTGCAAGGCTTCGGGAGACCCAGAGTTTCTCGCCCTTTAGA 10127
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Qy 900 TCCAAACTTGGAGCAACCCGGAGTCTGGATCTCTGGGAAGTCTCTACAGTGTCTCTGCGGTTG 959
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 Db
 Qy 960 TGCCGGGGGGCCCCAGGTCTCGAGGGGACCAAGTGGCCGTGTGGC 1001
 10188 TGCCGGGGGGCCCCAGGTCTCGAGGGGACCAAGTGGCCGTGTGGC 10229
 Db

RESULT 9

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US-08-974-549A-6
; Sequence 6, Application US/08974549A
; Patent No. 6186178
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Nakagura, Toru
; APPLICANT: Nagamer, Joachim
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:

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Query Match	93.0%	Score 930.8	DB 3	Length 4335
Best Local Similarity	99.1%	Pred. No. 9.7e-267		
Matches 999	Conservative 0	Mismatches 2	Indels 7	Gaps 6
QY	1	GGCTGGGATTTACAGGACACCGCCACCATGCCAGCTAAATTTTTTGTATTTTTAGTAGAGA	60	
Db	438	GGCTGGGATTTACAGGACACCGCCACCATGCCAGCTAAATTTTTTGTATTTTTAGTAGAGA	497	
QY	61	CGGGGGTGGGGGTGGGGTTCCACATGTTGGCCAGGCTGGTCTCGAACTTCTGACCTCAGA	120	
Db	498	CGGGGGTGGGGGTGGGGTTCCACATGTTGGCCAGGCTGGTCTCGAACTTCTGACCTCAGA	557	
QY	121	TGATCCACCTGCTCTGCTCTCTTAAAGTGTCTGGGATTAACAGGTGTGAGCCACCATGCCCCA	180	
Db	558	TGATCCACCTGCTCTGCTCTCTTAAAGTGTCTGGGATTAACAGGTGTGAGCCACCATGCCCCA	617	
QY	181	GCTCAGAAATTTACTCTGTTTTAGAAACATCTGGGCTCTGAGGTAGGAAGCTCACCCCACTCA	240	
Db	618	GCTCAGAAATTTACTCTGTTTTAGAAACATCTGGGCTCTGAGGTAGGAAGCTCACCCCACTCA	677	
QY	241	AGTGTGTGGTGTGTTTTAAGCCAATGATAGAAATTTTTTTATTTGTTGTAGAACTCTTTGA	300	
Db	678	AGTGTGTGGTGTGTTTTAAGCCAATGATAGAAATTTTTTTATTTGTTGTAGAACTCTTTGA	737	
QY	301	TGTTTTACACTGTGATGACTAAGACATCATCAGCTTTTCAAAGACACACTTAACCTGACCC	360	
Db	738	TGTTTTACACTGTGATGACTAAGACATCATCAGCTTTTCAAAGACACACTTAACCTGACCC	797	
QY	361	ATAATACTGGGGTGTCTTCTGGGTATCAGCGATCTTCATTTGATGCGGGAGGGTTTCC	420	
Db	798	ATAATACTGGGGTGTCTTCTGGGTATCAGCGATCTTCATTTGATGCGGGAGGGTTTCC	857	
QY	421	TCGCCATGCACATGTGTGTTAAATTTACTCCAGCAATACTCTCGTCTCCATTCTTCTCTTC	480	
Db	858	TCGCCATGCACATGTGTGTTAAATTTACTCCAGCAATACTCTCGTCTCCATTCTTCTCTTC	917	
QY	481	CCTCTTTTAAAAATTGTTTTTCTATGTGGCTTCTCTGCAGAGAACAGGTGAAGCTTACA	540	
Db	918	CCTCTTTTAAAAATTGTTTTTCTATGTGGCTTCTCTGCAGAGAACAGGTGAAGCTTACA	977	
QY	541	ACTTAACTTTTGTGGAAACAAATTTTCCAAACCGCCCTTTGGCCCTAGTGGCAGAGACAA	600	
Db	978	ACTTAACTTTTGTGGAAACAAATTTTCCAAACCGCCCTTTGGCCCTAGTGGCAGAGACAA	1037	
QY	601	TTCAACAACACAGCCCTTTTAAAGGCTTAGGGATCACTAAGGGGATTTTCTAGAAGAGCG	660	
Db	1038	TTCAACAACACAGCCCTTTTAAAGGCTTAGGGATCACTAAGGGGATTTTCTAGAAGAGCG	1097	
QY	661	ACCCTGAATCC-TAAGTATTTTACAAGACGAGGCTTAACCTCCAGCGAGCGTGAACGCCACG	719	

Db 1098 ACCGTAATCTTAAGTATTACAGAGCAGGCTAACTCCAGCGAGCGTGACAGCCAG 1157
Qy 720 GGAGGGTGGAGGCTCTTCAAAAGCTA-CCTCCATAAATAAGC-AAATTCCTCGGC 776
Db 1158 GGAGGGTGGAGGCTCTTCAAAAGCTAAGCTTCAATAAATAAGCAAAATTCCTCGGC 1217
Qy 777 AGTTTCT-GAAAGTAGAAAGGTT-ACATTTAAGGTTGCGTTTGTAGCATTTTCAGTGT 834
Db 1218 AGTTTCTGGAAGTAGGAAGTTAACTTTAAGTTGCGTTTGTAGCATTTTCAGTGT 1277
Qy 835 TGCCGACTCAGCT-ACAGCATCTCTGCAAGGCTTCGGAGACCCAGAGTTTTCGCC 893
Db 1278 TGCCGACTCAGCTAAACAGCATCTCTGCAAGGCTTCGGAGACCCAGAGTTTTCGCC 1337
Qy 894 CTTAGATCCAACTTGAGCAACCGGAGTCTGGATCTCTGGGAAGTCTCAGCTGTCTG 953
Db 1338 CTTAGATCCAACTTGAGCAACCGGAGTCTGGATCTCTGGGAAGTCTCAGCTGTCTG 1397
Qy 954 CGGTTGTGCCGGGCCCCAGGCTCTGGAGGGACCAAGTGGCCGTGTGGC 1001
Db 1398 CGGTTGTGCCGGGCCCCAGGCTCTGGAGGGACCAAGTGGCCGTGTGGC 1445

RESULT 10

US-09-721-456-6

; Sequence 6, Application US/09721456

; Patent No. 6617110

; GENERAL INFORMATION:

; APPLICANT: Cech, Thomas R.

; Lingner, Joachim

; Nakamura, Toru

; Chapman, Karen B.

; Morin, Gregg B.

; Harley, Calvin B.

; Andrews, William H.

; TITLE OF INVENTION: Human Telomerase Catalytic Subunit

; NUMBER OF SEQUENCES: 727

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, Eighth Floor

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/721,456

; FILING DATE: 22-No. 6617110-2000

; CLASSIFICATION: <Unknown>

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: US/08/974,549A

; FILING DATE: 19-NOV-1997

; APPLICATION NUMBER: US 08/724,643

; FILING DATE: 01-OCT-1996

; APPLICATION NUMBER: US 08/844,419

; FILING DATE: 18-APR-1997

; APPLICATION NUMBER: US 08/846,017

; FILING DATE: 25-APR-1997

; APPLICATION NUMBER: US 08/851,843

; FILING DATE: 06-MAY-1997

; APPLICATION NUMBER: US 08/854,050

; FILING DATE: 09-MAY-1997

; APPLICATION NUMBER: US 08/911,312

; FILING DATE: 14-AUG-1997

; APPLICATION NUMBER: US 08/912,951

; FILING DATE: 14-AUG-1997

; APPLICATION NUMBER: US 08/915,503

; FILING DATE: 14-AUG-1997

; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4335 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..4335
; OTHER INFORMATION: /note= "genomic DNA insert of pGRN144"
; FEATURE:
; NAME/KEY: intron
; LOCATION: 2715..2818
; OTHER INFORMATION: /note= "intron 1"
; FEATURE:
; NAME/KEY: intron
; LOCATION: 4173..4326
; OTHER INFORMATION: /note= "intron 2"
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-721-456-6

Query Match 93.0%; Score 930.8; DB 3; Length 4335;

Best Local Similarity 99.1%; Pred. No. 9.7e-267;

Matches 999; Conservative 0; Mismatches 2; Indels 7; Gaps 6;

Qy 1 GGCTGGGATTACAGGCACCCGCCACCATGCCAGCTAAATTTTGTATTTTAGTAGAGA 60
Db 438 GGCTGGGATTACAGGCACCCGCCACCATGCCAGCTAAATTTTGTATTTTAGTAGAGA 497
Qy 61 CGGGGGTGGGGTGGGGTTACCATGTGTGGCAGGTGCTCGAACTTCTGACCTCAGA 120
Db 498 CGGGGGTGGGGTGGGGTTACCATGTGTGGCAGGTGCTCGAACTTCTGACCTCAGA 557
Qy 121 TGATCCACCTGCTCTGCTTAAAGTCTGGGTTACAGGTGTGAGCCACCATGCCCA 180
Db 558 TGATCCACCTGCTCTGCTTAAAGTCTGGGTTACAGGTGTGAGCCACCATGCCCA 617
Qy 181 GCTCAGAAATTTACTCTGTTTAAAGAACATCTGGGTCTGAGGTAGGAAGCTCACCCCACTCA 240
Db 618 GCTCAGAAATTTACTCTGTTTAAAGAACATCTGGGTCTGAGGTAGGAAGCTCACCCCACTCA 677
Qy 241 AGTGTGTGGTGTGTTTAAAGCAATGATAGAAATTTTATTTTGTGTAGAACACTCTTGA 300
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Qy 361 ATAATACCTGGGGTGTCTTCTGGGTATCAGCATCTTCAATGAAATCCCGGAGGCGTTTCC 420
Db 798 ATAATACCTGGGGTGTCTTCTGGGTATCAGCATCTTCAATGAAATCCCGGAGGCGTTTCC 857
Qy 421 TCGCCATGCACATGGTGTAAATTAATCTCCAGCATAAATCTTCTGCTTCCATTTCTCTTC 480
Db 858 TCGCCATGCACATGGTGTAAATTAATCTCCAGCATAAATCTTCTGCTTCCATTTCTCTTC 917
Qy 481 CCTCTTTTAAATTTGTGTTTTCTATGTGGCTTCTCTCAGAGAACCAAGTGTAGCTACA 540
Db 918 CCTCTTTTAAATTTGTGTTTTCTATGTGGCTTCTCTCAGAGAACCAAGTGTAGCTACA 977

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Qy 541 ACTTAACTTTTGGGAACAAATTTTCAAACCGCCCTTTGCCCTAGTGGCAGACAA 600
Db 978 ACTTAACTTTTGGGAACAAATTTTCAAACCGCCCTTTGCCCTAGTGGCAGACAA 1037
Qy 601 TTCAAAACACAGCCCTTTTAAAAAGGCTTAGGGATCATAAGGGGATTTCTAGAAAGAGCG 660
Db 1038 TTCAAAACACAGCCCTTTTAAAAAGGCTTAGGGATCATAAGGGGATTTCTAGAAAGAGCG 1097
Qy 661 ACCGTAATCC-TAAGTATTTACAAAGCAGGCTTAACCTCCAGGAGCGGTGACAGCCGAG 719
Db 1098 ACCGTAATCCTTAAGTATTTACAAAGCAGGCTTAACCTCCAGGAGCGGTGACAGCCGAG 1157
Qy 720 GGAGGGTGGCAGGCGCTGTCAAATGCTA--GCTCCATAAATAAAGC-AAATTCCTCCGGC 776
Db 1158 GGAGGGTGGCAGGCGCTGTCAAATGCTAAGTTCATTAATAAGAAATTTCTCCGGC 1217
Qy 777 AGTTTCT-GAAAGTAGAAAGGTT-ACATTTAAGGTTGCGTTGTTAGTCAATTTCAAGTGT 834
Db 1218 AGTTTCTGGAAGTAGAAAGGTTTAAATTTAAGGTTGCGTTGTTAGTCAATTTCAAGTGT 1277
Qy 835 TGGCACTCAGCT-ACAGCATCCTCGCAAGCCCTCGGAGACCCAGAAAGTTTCTGCC 893
Db 1278 TGGCACTCAGCTAAACAGCATCCTCGCAAGCCCTCGGAGACCCAGAAAGTTTCTGCC 1337
Qy 894 CTTAGATCCAAACTTGAGCAACCGGAGTCTGGATTCTCGGAAGTCTCAGCTGTCTG 953
Db 1338 CTTAGATCCAAACTTGAGCAACCGGAGTCTGGATTCTCGGAAGTCTCAGCTGTCTG 1397
Qy 954 CGGTTGTGCGGGGCCCCAGGCTCTGGAGGGGACACAGTGGCGCGTGTGGC 1001
Db 1398 CGGTTGTGCGGGGCCCCAGGCTCTGGAGGGGACACAGTGGCGCGTGTGGC 1445
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RESULT 11

US-09-956-335-2/c

; Sequence 2, Application US/09956335

; Patent No. 6627190

; GENERAL INFORMATION:

; APPLICANT: WOLD, William

; APPLICANT: TOTH, Karoly

; APPLICANT: KUPPASWAMI, Mohan

; APPLICANT: DORONIN, Konsantin

; TITLE OF INVENTION: RECOMBINANT ADENOVIRUS VECTORS THAT ARE

; FILE REFERENCE: 16153-8394

; CURRENT APPLICATION NUMBER: US/09/956,335

; CURRENT FILING DATE: 2001-09-19

; NUMBER OF SEQ ID NOS: 3

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 2

; LENGTH: 35871

; TYPE: DNA

; ORGANISM: Adenovirus

US-09-956-335-2

Query Match 67.7%; Score 677.8; DB 3; Length 35871;

Best Local Similarity 99.7%; Pred. No. 5.7e-191;

Matches 679; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy 321 AAGCATCATCAGCTTTTCAAAGACACACTAACTGCAACCCATATACTATCTGGGGTGTCTCT 380
Db 35713 AAGTAATCATCAGCTTTTCAAAGACACACTAACTGCAACCCATATACTATCTGGGGTGTCTCT 35654
Qy 381 GGGTATCAGCGATCTTCATTGAATGCCGGAGGCGTTTCTCGCATGCACATGGTGTTA 440
Db 35653 GGGTATCAGCGATCTTCATTGAATGCCGGAGGCGTTTCTCGCATGCACATGGTGTTA 35594
Qy 441 ATTACTCCAGCATATCTTCGCTTCCATTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 500
Db 35593 ATTACTCCAGCATATCTTCGCTTCCATTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 35534
Qy 501 TCTATGTTGGCTTCTCTGCAAGAACACAGTGTAGCTTACAACTTAACTTTTGTGGAAACA 560
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Db 35533 TCTATGTTGGCTTCTCTGCAAGAACACAGTGTAGCTTACAACTTAACTTTTGTGGAAACA 35474
Qy 561 AATTTTCCAAACCGCCCTTTTGGCCCTAGTGGCAGAGCAATTCACAAACACAGCCCTTTTA 620
Db 35473 AATTTTCCAAACCGCCCTTTTGGCCCTAGTGGCAGAGCAATTCACAAACACAGCCCTTTTA 35414
Qy 621 AAAAGGCTTAGGGATCATAAAGGGGATTTCTAGAAAGCGACCCGTAATCCTAGTATTTT 680
Db 35413 AAAAGGCTTAGGGATCATAAAGGGGATTTCTAGAAAGCGACCCGTAATCCTAGTATTTT 35354
Qy 681 ACAAGACGAGGCTAAACCTCCAGCGAGCGTGACAGCCCGAGGGAGGGTGCAGAGCCCTGTTC 740
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Qy 741 AATGCTAGCTCCATAATAATAAGCAATTTCTCCGGCAGTTTCTGAAAGTAGGAAGGTTA 800
Db 35293 AATGCTAGCTCCATAATAATAAGCAATTTCTCCGGCAGTTTCTGAAAGTAGGAAGGTTA 35234
Qy 801 CATTTAAGGTTGCGTTTGTAGCATTTTCAGTGTTCGCGACCTCAGCTACAGCATCCCTG 860
Db 35233 CATTTAAGGTTGCGTTTGTAGCATTTTCAGTGTTCGCGACCTCAGCTACAGCATCCCTG 35174
Qy 861 CAAGGCTCCTCGGAGACCCAGAAAGTTTCTCGCCCTTAGATCCAAACTTGAGCAACCCGGA 920
Db 35173 CAAGGCTCCTCGGAGACCCAGAAAGTTTCTCGCCCTTAGATCCAAACTTGAGCAACCCGGA 35114
Qy 921 GTCTGATTCCTGGGAAGTCTCAGCTGTCTCGGGTGTGTCGGGGCCCCAGGTCTGGGA 980
Db 35113 GTCTGATTCCTGGGAAGTCTCAGCTGTCTCGGGTGTGTCGGGGCCCCAGGTCTGGGA 35054
Qy 981 GGGGACCAAGTGGCGGTGTGGC 1001
Db 35053 GGGGACCAAGTGGCGGTGTGGC 35033
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RESULT 12

US-09-956-335-1/c

; Sequence 1, Application US/09956335

; Patent No. 6627190

; GENERAL INFORMATION:

; APPLICANT: WOLD, William

; APPLICANT: TOTH, Karoly

; APPLICANT: KUPPASWAMI, Mohan

; APPLICANT: DORONIN, Konsantin

; TITLE OF INVENTION: RECOMBINANT ADENOVIRUS VECTORS THAT ARE

; FILE REFERENCE: 16153-8394

; CURRENT APPLICATION NUMBER: US/09/956,335

; CURRENT FILING DATE: 2001-09-19

; NUMBER OF SEQ ID NOS: 3

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1

; LENGTH: 35978

; TYPE: DNA

; ORGANISM: Adenovirus

US-09-956-335-1

Query Match 67.7%; Score 677.8; DB 3; Length 35978;

Best Local Similarity 99.7%; Pred. No. 5.7e-191;

Matches 679; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy 321 AAGCATCATCAGCTTTTCAAAGACACACTAACTGCAACCCATATACTATCTGGGGTGTCTCT 380
Db 35820 AAGTAATCATCAGCTTTTCAAAGACACACTAACTGCAACCCATATACTATCTGGGGTGTCTCT 35761
Qy 381 GGGTATCAGCGATCTTCATTGAATGCCGGAGGCGTTTCTCGCATGCACATGGTGTTA 440
Db 35760 GGGTATCAGCGATCTTCATTGAATGCCGGAGGCGTTTCTCGCATGCACATGGTGTTA 35701
Qy 441 ATTACTCCAGCATATCTTCGCTTCCATTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 500
Db 35700 ATTACTCCAGCATATCTTCGCTTCCATTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 35641
```

Qy 501 TCTATGTTGGCTTCTCTGAGAGAACAGTGTAACTTAACTTTTGTGGACA 560
Db |||||||
35640 TCTATGTTGGCTTCTCTGAGAGAACAGTGTAACTTAACTTTTGTGGACA 35581
Qy 561 AATTTTCAAACCGCCCTTTGGCCCTAGTGGAGAGACAATTCACAAACACAGCCCTTTA 620
Db |||||||
35580 AATTTTCAAACCGCCCTTTGGCCCTAGTGGAGAGACAATTCACAAACACAGCCCTTTA 35521
Qy 621 AAAAGGCTTAGGGATCACTAAGGGGATTTCTAGAGAGCGACCCGTAATCCTAAGTATTT 680
Db |||||||
35520 AAAAGGCTTAGGGATCACTAAGGGGATTTCTAGAGAGCGACCCGTAATCCTAAGTATTT 35461
Qy 681 ACAAGACGAGCTTAACCTCCAGCGAGCGTGAAGCCAGGAGGGTGGAGGCGCTGTTC 740
Db |||||||
35460 ACAAGACGAGCTTAACCTCCAGCGAGCGTGAAGCCAGGAGGGTGGAGGCGCTGTTC 35401
Qy 741 AATGCTAGCTCATAAATAAAGCAATTTCTCCGGCAGTTCCTGAAAGTAGGAAGGTTA 800
Db |||||||
35400 AATGCTAGCTCATAAATAAAGCAATTTCTCCGGCAGTTCCTGAAAGTAGGAAGGTTA 35341
Qy 801 CATTTAAGGTTGCGTTTCTAGCAATTTCCAGTGTGTTCCGACCTCAGCTACAGCATCCCTG 860
Db |||||||
35340 CATTTAAGGTTGCGTTTCTAGCAATTTCCAGTGTGTTCCGACCTCAGCTACAGCATCCCTG 35281
Qy 861 CAAGGCTCGGGAGACCCAGAAAGTTTCTCGCCCTTAGATCCAACTTGAGCAACCCGGA 920
Db |||||||
35280 CAAGGCTCGGGAGACCCAGAAAGTTTCTCGCCCTTAGATCCAACTTGAGCAACCCGGA 35221
Qy 921 GTCTGGATCTCGGAAGTCTCAGCTGTCTGCGGTTGTCGCGGGCCCCAGGTCGTGA 980
Db |||||||
35220 GTCTGGATCTCGGAAGTCTCAGCTGTCTGCGGTTGTCGCGGGCCCCAGGTCGTGA 35161
Qy 981 GGGGACCAAGTGGCGTGTGGC 1001
Db |||||||
35160 GGGGACCAAGTGGCGTGTGGC 35140

RESULT 13

US-09-956-335-3/c
; Sequence 3, Application US/09956335
; Patent No. 6627190
; GENERAL INFORMATION:
; APPLICANT: WOLD, William
; APPLICANT: TOTH, Karoly
; APPLICANT: KUPPASHWAMI, Mohan
; APPLICANT: DORONIN, Ronbentim
; TITLE OF INVENTION: RECOMBINANT ADENOVIRUS VECTORS THAT ARE
; FILE REFERENCE: 16153-8394
; CURRENT APPLICATION NUMBER: US/09/956,335
; CURRENT FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 3
; TYPE: DNA
; ORGANISM: Adenovirus
US-09-956-335-3

Query Match 67.5%; Score 676; DB 3; Length 1677;
Best Local Similarity 100.0%; Pred. No. 4.8e-191;
Matches 576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 326 ATCATCAGCTTTTCAAAGACACACTAACTGACCCCATTAATACTGGGGTGTCTCTGGGTA 385
Db |||||||
1676 ATCATCAGCTTTTCAAAGACACACTAACTGACCCCATTAATACTGGGGTGTCTCTGGGTA 1617
Qy 386 TCAGGATCTTCATTAATGTCGGGAGCGGTTCTCCGCCATGCACATGGTGTAAATTAC 445
Db |||||||
1616 TCAGGATCTTCATTAATGTCGGGAGCGGTTCTCCGCCATGCACATGGTGTAAATTAC 1557
Qy 446 TCCAGCAATATCTCTGCTTCATTTCTCTCCCTTTTAAATTTGTTTCTAT 505
Db |||||||

Db 1556 TCCAGCAATATCTCTGCTTCCATTTCTCTCTTCCCTCTTTTAAATTTGTTTCTAT 1497
Qy 506 GTTGGCTTCTCTGAGAGAACAGTGTAACTTAACTTTTGTGGACAATTT 565
Db |||||||
1496 GTTGGCTTCTCTGAGAGAACAGTGTAACTTAACTTTTGTGGACAATTT 1437
Qy 566 TCCAAAACCGCCCTTTTGGCCCTAGTGGAGAGACAATTCACAAACACAGCCCTTTAAAAAG 625
Db |||||||
1436 TCCAAAACCGCCCTTTTGGCCCTAGTGGAGAGACAATTCACAAACACAGCCCTTTAAAAAG 1377
Qy 626 GCTTAGGATCACTAAGGGGATTTCTAGAGAGCGACCCGTAATCCTAAGTATTTACAAG 685
Db |||||||
1376 GCTTAGGATCACTAAGGGGATTTCTAGAGAGCGACCCGTAATCCTAAGTATTTACAAG 1317
Qy 686 ACGAGGCTTAACCTCCAGCGAGCGTGACAGCCAGGAGGGTGGAGGCGCTGTTCAAAATGC 745
Db |||||||
1316 ACGAGGCTTAACCTCCAGCGAGCGTGACAGCCAGGAGGGTGGAGGCGCTGTTCAAAATGC 1257
Qy 746 TAGCTCCATAAATAAAGCAATTTCTCCGGCAGTTCCTGAAAAGTAGGAAGGTTACATTT 805
Db |||||||
1256 TAGCTCCATAAATAAAGCAATTTCTCCGGCAGTTCCTGAAAAGTAGGAAGGTTACATTT 1197
Qy 806 AAGTGGCTTTGTAGCAATTTCTAGTGTTCGCGACCTCAGCTACAGCATCCCTGCAAGG 865
Db |||||||
1196 AAGTGGCTTTGTAGCAATTTCTAGTGTTCGCGACCTCAGCTACAGCATCCCTGCAAGG 1137
Qy 866 CCTCGGAGACCCAGAAAGTTTCTCGCCCTTAGATCCAACTTGAGCAACCCGAGTCTG 925
Db |||||||
1136 CCTCGGAGACCCAGAAAGTTTCTCGCCCTTAGATCCAACTTGAGCAACCCGAGTCTG 1077
Qy 926 GATTCTCTGGGAAGTCTCAGCTGTCTCGCGTGTGCGGGGCCCCAGGTCTGGAGGGGA 985
Db |||||||
1076 GATTCTCTGGGAAGTCTCAGCTGTCTCGCGTGTGCGGGGCCCCAGGTCTGGAGGGGA 1017
Qy 986 CCAGTGGCGGTGTGGC 1001
Db |||||||
1016 CCAGTGGCGGTGTGGC 1001

RESULT 14

US-09-244-438-22
; Sequence 22, Application US/09244438
; Patent No. 6777203
; GENERAL INFORMATION:
; APPLICANT: Morin, Gregg B.
; APPLICANT: Lichtsteiner, Serge
; APPLICANT: Vasserot, Alain
; APPLICANT: Adams, Robert R.
; APPLICANT: Geron Corporation
; TITLE OF INVENTION: Telomerase Reverse Transcriptase Transcriptional
; FILE REFERENCE: 019/246P
; CURRENT APPLICATION NUMBER: US/09/244,438
; CURRENT FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 22
; LENGTH: 497
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Human TERT promoter
US-09-244-438-22

Query Match 49.7%; Score 497; DB 3; Length 497;
Best Local Similarity 100.0%; Pred. No. 5.6e-138;
Matches 497; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 444 ACTCAGCATTAATCTCTGCTTCCATTTCTCTTCCCTCTTTTAAATTTGTTTCT 503
Db 1 ACTCAGCATTAATCTCTGCTTCCATTTCTCTTCCCTCTTTTAAATTTGTTTCT 60
Qy 504 ATGTTGGCTTCTCTGCAGAGAACAGTGTAGCTACAACTTAACTTTTGTGGACAAT 563
Db |||||||


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Qy 659 CGACCCGTAATCCTAAGTATTACAAGACGAGGCTAACCTCAGCGAGCGTGACAGCCCA 718
Db 1132 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
Qy 719 GGGAGGGTGCAGGCGCTGTTCAAAATGCTAGTCCATAAATAAGCAAATTTCTCCGGCAG 778
Db 1192 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
Qy 779 TTTCTGAAAGTAGGAAAGGTTACATTTAAGGTTGCGTTGTTAGCATTTTCAGTGTTCGCC 838
Db 1252 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
Qy 839 GACCTCAGCTACAGCATCCCTGCAAGGCTCGGAGAGACCAGAAAGTTTCTCGCCCTTAG 898
Db 1312 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
Qy 899 ATCAAACCTTGAGCAACCCGAGTCTGGAATTCCTGGGAAAGTCTCAGCTGCTGCGGTT 958
Db 1372 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
Qy 959 GTGCGGGGGCCCGAGTCTGGAG 981
Db 1432 GNNRGAGGGGCCANGRAGGGG 1454
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Search completed: January 10, 2006, 19:47:34
Job time : 208 secs

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OM nucleic - nucleic search, using sw model

Run on: January 10, 2006, 05:46:59 ; Search time 690.667 Seconds
(without alignments)
9659.301 Million cell updates/sec

Title: US-09-615-039-1_COPY_11500_12500

Perfect score: 1001

Sequence: 1 ggctgggattacagacc.....gggaccagtggcgtgtggc 1001

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_21.*

- 1: geneseq1980s.*
- 2: geneseq1990s.*
- 3: geneseq2000s.*
- 4: geneseq2001as.*
- 5: geneseq2001bs.*
- 6: geneseq2002as.*
- 7: geneseq2002bs.*
- 8: geneseq2003as.*
- 9: geneseq2003bs.*
- 10: geneseq2003cs.*
- 11: geneseq2003ds.*
- 12: geneseq2004as.*
- 13: geneseq2004bs.*
- 14: geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1001	100.0	15418	3	AA63785 Nucleotide
2	1001	100.0	15418	6	Aa138601 Human TER
3	1001	100.0	15418	6	AB54997 Lambda cl
4	1001	100.0	15418	6	Aa138595 DNA of pl
5	1001	100.0	15418	10	Adc21253 Lambda cl
6	989	98.8	3962	4	Aa41091 Telomeras
7	989	98.8	4356	13	Adu82633 Human hTE
8	988.6	98.8	4293	14	Adv23865 Human hTE
9	972.8	97.2	5491	13	Adu82631 Human hTE
10	972.8	97.2	51552	6	Aa96607 DNA encod
11	971.8	97.1	5126	2	Aax88272 Human cat
12	956	95.5	2501	14	Adv97952 Human tum
13	954.4	95.3	7928	14	Aa18025 Human gyn
14	930.8	93.0	4335	2	Aav16379 Human tel
15	677.8	67.7	35871	6	Aad27972 Recombina
16	677.8	67.7	35978	6	Aad27971 Recombina
17	676	67.5	1677	6	Aad27973 Recombina
18	676	67.5	2043	14	Adv23882 Human hTE
19	643.2	64.3	4356	6	Ab192335 Chemicall

20	636	63.5	4356	6	ABL92334	Ab192334 Chemicall
21	623.8	62.3	2501	14	ADV98043	Adv98043 Bisulfite
22	623.4	62.3	2501	14	ADV98042	Adv98042 Bisulfite
23	622.2	62.2	7928	14	AEA18047	Aea18047 Converted
24	620.2	62.0	7928	14	AEA18046	Aea18046 Converted
25	588.6	58.8	2501	14	ADV98137	Adv98137 Bisulfite
26	588.6	58.8	7928	14	AEA18067	Aea18067 Converted
27	588.2	58.8	2501	14	ADV98136	Adv98136 Bisulfite
28	586.6	58.6	7928	14	AEA18066	Aea18066 Converted
29	205.6	20.5	1404	6	AD22343	Ad22343 Chemicall
30	195.6	19.5	1404	6	AD22344	Ad22344 Chemicall
31	136.4	13.6	158980	13	ADZ44537	Adz44537 Human bre
32	134.2	13.4	7268	4	AAK85177	Aak85177 Human imm
33	134.2	13.4	18596	4	AAF31109	Aaf31109 Thymidyla
34	134.2	13.4	18596	5	AAC91215	Aac91215 Human thy
35	134.2	13.4	18596	6	ABL67927	Ab167927 Ovary can
36	134.2	13.4	18596	6	ABL62854	Ab162854 Breast ca
37	134.2	13.4	18596	6	ABL63078	Ab163078 Breast ca
38	134.2	13.4	18596	6	ABK43334	Abk43334 Human Thy
39	134.2	13.4	18596	6	ABN95092	Abn95092 Gene #159
40	134.2	13.4	18596	14	AEA63667	Aea63667 Thymidyla
41	134.2	13.4	45716	6	ABA93401	Ab93401 Human rTS
42	134.2	13.4	45989	6	ABA93402	Ab93402 Human rTS
43	132.8	13.3	196686	11	ACN44170	Acn44170 Human gen
44	132.2	13.2	24295	12	ADP31706	Adp31706 Human oes
45	131.4	13.1	69648	12	ADQ97934	Adq97934 Human can

ALIGNMENTS

RESULT 1

AAA63785

ID AAA63785 standard; DNA; 15418 BP.

XX AAA63785;

DT 04-DEC-2000 (first entry)

XX Nucleotide sequence of the human TERT promoter and gene from pGRN142.

XX Telomerase reverse transcriptase; TERT; promoter; telomerase complex;

XX telomere length; hyperplasic disease; cancer; oncolytic virus;

XX cis-acting transcriptional control sequence; viral replication;

XX cell proliferation; aging; immunological disorder; infertility; ss.

XX Homo sapiens.

XX WO200046355-A2.

XX 10-AUG-2000.

XX 04-FEB-2000; 2000WO-US003104.

XX 04-FEB-1999; 99US-00244438.

XX (GERO-) GERON CORP.

XX Morin GB, Lichtsteiner S, Vasserot A, Adams R, Cardozo LM;

XX Lebkowski JS;

XX WPI; 2000-532898/48.

XX New polynucleotides comprising cis-acting transcriptional control sequences, e.g. promoter sequence, of telomerase reverse transcriptase genes, useful in the treatment of cancer.

XX Claim 9; Page 58-61; 63pp; English.

XX The present sequence represents the human telomerase reverse transcriptase (TERT) promoter and gene. TERT is part of the telomerase complex responsible for maintaining telomere length and increasing replicative capacity of progenitor cells. Telomerase activity is turned

off in mature differentiated cells, but is turned back on again in hyperplastic diseases, including many cancers. The polynucleotide comprises cis-acting transcriptional control sequences, e.g. promoter sequences. These promoter sequences are used to produce oncolytic viruses, in which a toxin or genetic element essential for viral replication is placed under the control of a TERT promoter. As a result, the virus replicates preferentially in cells expressing TERT, and selectively lyses cancer cells. The oncolytic viruses are useful for treating cancer in humans or animals. The TERT promoter sequences are useful in the treatment of cancer and other diseases of cell proliferation such as degenerative and aging processes and diseases of aging, immunological disorders, or infertility

XX
SQ Sequence 15418 BP; 4518 A; 3797 C; 3765 G; 3338 T; 0 U; 0 Other;

Query Match 100.0%; Score 1001; DB 3; Length 15418;
Best Local Similarity 100.0%; Pred. No. 6.4e-291;
Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCTGGGATTACAGGACCGCCGACCATGCCAGCTAAATTTTGTATTTTGTAGTAGAGA 60
DB 11500 GGCTGGGATTACAGGACCGCCGACCATGCCAGCTAAATTTTGTATTTTGTAGTAGAGA 11559
QY 61 CGGGGGTGGGGGTTCACCATGTTGGCCAGGCTGGTCTCGAATCTCTGACCTCAGA 120
DB 11560 CGGGGGTGGGGGTTCACCATGTTGGCCAGGCTGGTCTCGAATCTCTGACCTCAGA 11619
QY 121 TGATCCACCTGCTCTGCCCTCTAAAGTGTGGGATTACAGGTGTGAGCCACCATGCCCA 180
DB 11620 TGATCCACCTGCTCTGCCCTCTAAAGTGTGGGATTACAGGTGTGAGCCACCATGCCCA 11679
QY 181 GCTCAGAAATTACTCTGTTAGAAACATCTGGGTCTGAGTAGGAAGCTCACCCTCA 240
DB 11680 GCTCAGAAATTACTCTGTTAGAAACATCTGGGTCTGAGTAGGAAGCTCACCCTCA 11739
QY 241 AGTGTCTGTGTTTAAAGCAATGATAGAAATTTTATTTTGTAGTAACTCTTTGA 300
DB 11740 AGTGTCTGTGTTTAAAGCAATGATAGAAATTTTATTTTGTAGTAACTCTTTGA 11799
QY 301 TGTTTTACCTGTGATGACTAAGACATCATCAGCTTTTCAAAGACACACTAAGTCACCC 360
DB 11800 TGTTTTACCTGTGATGACTAAGACATCATCAGCTTTTCAAAGACACACTAAGTCACCC 11859
QY 361 ATAATCTGGGGTCTCTTGGGTATCAGCATCTTCAATGAATCCGGGAGGGTTTC 420
DB 11860 ATAATCTGGGGTCTCTTGGGTATCAGCATCTTCAATGAATCCGGGAGGGTTTC 11919
QY 421 TCGCATGCATGGTGTAAATTAATCTCAGCATATCTTCTGCTTCCATTTCTTCTTC 480
DB 11920 TCGCATGCATGGTGTAAATTAATCTCAGCATATCTTCTGCTTCCATTTCTTCTTC 11979
QY 481 CCTCTTTAAATTTGTTTCTATGTTGGCTTCTTCGAGAGAACAGTGTAGTACA 540
DB 11980 CCTCTTTAAATTTGTTTCTATGTTGGCTTCTTCGAGAGAACAGTGTAGTACA 12039
QY 541 ACTTAATCTTTTGGAAACAAATTTTCAAACCGCCCTTGGCCCTAGTGGCAGACAA 600
DB 12040 ACTTAATCTTTTGGAAACAAATTTTCAAACCGCCCTTGGCCCTAGTGGCAGACAA 12099
QY 601 TTCACAAACACAGCCCTTTAAAGAGGTAGGGATCACTAAGGGGATTTCTAGAAAGCG 660
DB 12100 TTCACAAACACAGCCCTTTAAAGAGGTAGGGATCACTAAGGGGATTTCTAGAAAGCG 12159
QY 661 ACCGTAATCTTAAGTATTTTAAAGACGAGCTTAACCTCCAGCGAGGCTGACAGCCGAG 720
DB 12160 ACCGTAATCTTAAGTATTTTAAAGACGAGCTTAACCTCCAGCGAGGCTGACAGCCGAG 12219
QY 721 GAGGGTCGAGGCTGTTTCAATCTAGTCCATAAATAAGCAATTTCTCCGGCAGTT 780
DB 12220 GAGGGTCGAGGCTGTTTCAATCTAGTCCATAAATAAGCAATTTCTCCGGCAGTT 12279
QY 781 TCTCAAAAGTAGAAAGGTTTCAATTTAAGTTGCGTTTGTAGCATTTTCAGTGTTCGCGA 840
DB 11500 GGCTGGGATTACAGGACCGCCGACCATGCCAGCTAAATTTTGTATTTTGTAGTAGAGA 11559

DB 12280 TCTGAAAGTAGGAAAGTTTACATTTTAAAGTTTGGTTTGTAGCATTTTCAGTGTTCGCGA 12339
QY 841 CCTCAGCTACAGCATCCCTGCAAGGCTTCGGAGAGCCAGAGTTTCTCGCCCTTAGAT 900
DB 12340 CCTCAGCTACAGCATCCCTGCAAGGCTTCGGAGAGCCAGAGTTTCTCGCCCTTAGAT 12399
QY 901 CCAAACTTGAGCAAAACCGGAGTCTGGATTCTCTGGGAAGTCTCAGCTGTCTCGGGTTGT 960
DB 12400 CCAAACTTGAGCAAAACCGGAGTCTGGATTCTCTGGGAAGTCTCAGCTGTCTCGGGTTGT 12459
QY 961 GCCGGGGCCCCAGGTCTGGAGGGGACCAGTGGCGGTGTG3C 1001
DB 12460 GCCGGGGCCCCAGGTCTGGAGGGGACCAGTGGCGGTGTG3C 12500

RESULT 2

AAL38601
ID AAL38601 standard; DNA; 15418 BP.

XX AAL38601;

XX 16-AUG-2002 (first entry)

XX Human TERT promoter and upstream sequence.

XX Cytostatic; glycosyltransferase; tumour; cell-surface carbohydrate;

KW tissue specific; transcriptional control element; cancer cell;

KW gene therapy; human TERT; telomerase reverse transcriptase; ds.

XX Homo sapiens.

XX WO200242468-A2.

XX 30-MAY-2002.

XX 26-NOV-2001; 2001WO-US044306.

XX 27-NOV-2000; 2000US-0253395P.

XX (GERO-) GERON CORP.

XX Schiff MJ;

XX WPI; 2002-479954/51.

XX New polynucleotide encoding glycosyltransferase enzymes including histo blood group transferase useful for treating conditions associated with hyperproliferation, such as cancers and other neoplasias.

PS Claim 9; Page 17-20; 49pp; English.

XX The invention relates to a polynucleotide comprising an encoding sequence for a glycosyltransferase, under control of a heterologous tumour specific or tissue specific transcriptional control element, where expression of the polynucleotide in a human cell causes the cell to express a cell-surface carbohydrate determinant to which some or all humans have a naturally occurring antibody. The polynucleotide of the invention is useful for killing cancer cells and for preparing a medicament for the treatment of cancer. The polynucleotide sequence of the invention can be used to treat disorders by gene therapy. This polynucleotide sequence represents the human TERT (telomerase reverse transcriptase) promoter and upstream sequence related to the invention

XX SQ Sequence 15418 BP; 4518 A; 3797 C; 3765 G; 3338 T; 0 U; 0 Other;

Query Match 100.0%; Score 1001; DB 6; Length 15418;

Best Local Similarity 100.0%; Pred. No. 6.4e-291;

Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCTGGGATTACAGGACCGCCGACCATGCCAGTAAATTTTGTATTTTGTAGTAGAGA 60

DB 11500 GGCTGGGATTACAGGACCGCCGACCATGCCAGTAAATTTTGTATTTTGTAGTAGAGA 11559

Qy	61	CGGGGTGGGGGTGGGGGTTCCACATGTTTGGCAGAGCTGGTCTCGAACTTCGTGACCTCAGA	120
Db	11560	CGGGGTGGGGGTGGGGGTTCCACATGTTTGGCAGAGCTGGTCTCGAACTTCGTGACCTCAGA	11619
Qy	121	TGATCCACCTGCCTCTCGCCCTCTTAAGTGCTGGGAATTACAGGTGTGAGCACCACTGCCCCA	180
Db	11620	TGATCCACCTGCCTCTCGCCCTCTTAAGTGCTGGGAATTACAGGTGTGAGGCCACCATGCCCA	11679
Qy	181	GCTCAGAAATTACTCTGTTTTAGAAAACATCTGGGTCTGAGGTAGGAAGTCAACCCACATCA	240
Db	11680	GCTCAGAAATTACTCTGTTTTAGAAAACATCTGGGTCTGAGGTAGGAAGTCAACCCACATCA	11739
Qy	241	AGTGTTGTGGTGTGTTTTAAGCCAATGATAGAAATTTTTTTTATTGTTGTAGAACACTCTTGA	300
Db	11740	AGTGTTGTGGTGTGTTTTAAGCCAATGATAGAAATTTTTTTTATTGTTGTAGAACACTCTTGA	11799
Qy	301	TGTTTTACACTGTGATGACTAAGACATCATCAGCTTTTCAAAGACAACACTAACTGCACCC	360
Db	11800	TGTTTTACACTGTGATGACTAAGACATCATCAGCTTTTCAAAGACAACACTAACTGCACCC	11859
Qy	361	ATAATACTGGGGTGTCTTCTGGGTATCAGCGATCTTCAATTGAATGCCGGAGGGGTTTCC	420
Db	11860	ATAATACTGGGGTGTCTTCTGGGTATCAGCGATCTTCAATTGAATGCCGGAGGGGTTTCC	11919
Qy	421	TCGCCATGACATGGGTGTAAATTACTCAGACATAATCTTCTGCTTCCATTTCTTCTTCTC	480
Db	11920	TCGCCATGACATGGGTGTAAATTACTCAGACATAATCTTCTGCTTCCATTTCTTCTTCTC	11979
Qy	481	CCTCTTTTTAAAAATTGTGTTTTTCTATGTTGCTTCTCTGAGAGAACCAAGTGTAGCTACA	540
Db	11980	CCTCTTTTTAAAAATTGTGTTTTTCTATGTTGCTTCTCTGAGAGAACCAAGTGTAGCTACA	12039
Qy	541	ACTTAACTTTTGTGGAACAAATTTTTCAAACCGCCCTTTGCCCTTAGTGGCAGAGACAA	600
Db	12040	ACTTAACTTTTGTGGAACAAATTTTTCAAACCGCCCTTTGCCCTTAGTGGCAGAGACAA	12099
Qy	601	TTCAAAACACAGCCCTTTAAAAAGGCTTAGGATCACTAAAGGGATTTCTAGAGAGCG	660
Db	12100	TTCAAAACACAGCCCTTTAAAAAGGCTTAGGATCACTAAAGGGATTTCTAGAGAGCG	12159
Qy	661	ACCGTAACTCCTAAGTATTTTACAAGACGAGGCTTAACCTCCAGCAGCGTGCAGACGCCAGG	720
Db	12160	ACCGTAACTCCTAAGTATTTTACAAGACGAGGCTTAACCTCCAGCAGCGTGCAGACGCCAGG	12219
Qy	721	GAGGGTCGAGGCCTGTGTTCAAATGCTAGCTCCAATAATAAGCAATTTCTCCTCCGACGTT	780
Db	12220	GAGGGTCGAGGCCTGTGTTCAAATGCTAGCTCCAATAATAAGCAATTTCTCCTCCGACGTT	12279
Qy	781	TCGTAAAGTAGGAAAGGTTACATTTAAGGTTGGGTTGTAGTACATTTAGTGTGTTGCCGA	840
Db	12280	TCGTAAAGTAGGAAAGGTTACATTTAAGGTTGGGTTGTAGTACATTTAGTGTGTTGCCGA	12339
Qy	841	CCTCAGCTACAGCATCCCTCGCAAGGCTCGGGAGACCCAGAAAGTTTCTCGCCCTTAGAT	900
Db	12340	CCTCAGCTACAGCATCCCTCGCAAGGCTCGGGAGACCCAGAAAGTTTCTCGCCCTTAGAT	12399
Qy	901	CCAAACTTGAGCAACCCGGAGTCTGGATTCTCTGGGAAGTCCCTCAGCTGTCTGCGGTTGT	960
Db	12400	CCAAACTTGAGCAACCCGGAGTCTGGATTCTCTGGGAAGTCCCTCAGCTGTCTGCGGTTGT	12459
Qy	961	GCCGGGGCCCAAGTCTGGAGGGGACCAAGTGGCCGTGTGCG	1001
Db	12460	GCCGGGGCCCAAGTCTGGAGGGGACCAAGTGGCCGTGTGCG	12500

RESULT 3

ABS54997

ID ABS54997 standard; DNA; 15418 BP.

AC ABS54997:

DT 10-DEC-2002 (first entry)

DE	Lambda clone containing human TERT genomic insert.
KX	Telomerase reverse transcriptase; TERT; replication-conditional virus;
KW	adenovirus replication gene; cancer cell; lung; pancreatic cancer;
KW	medulloblastoma; cervical carcinoma; fibrosarcoma; osteosarcoma;
KW	cytolysis; replication defective adenovirus vector; congenital defect;
KW	proinflammatory; antiinflammatory; heterologous effector gene;
KW	cancer therapy; cyclostatic; gene therapy; lambda clone; human; ds.
XX	
XX	Bacteriophage lambda.
OS	Homo sapiens.
OS	Synthetic.
XX	
XX	Key
PH	Location/Qualifiers
FT	1. .43
FT	misc_feature
FT	/*tag= a
FT	/note= "From Lambda clone"
FT	44. .15375
FT	misc_feature
FT	/*tag= b
FT	/note= "Human telomerase reverse transcriptase (hTERT)
FT	sequence including the hTERT promoter and upstream
FT	sequence"
FT	15376. .15418
FT	misc_feature
FT	/*tag= c
FT	/note= "Prom Lambda clone"
XX	
XX	WO200253760-A2.
FN	
XX	
XX	11-JUL-2002.
PD	
XX	
XX	17-DEC-2001; 2001WO-US048785.
PF	
XX	
XX	18-DEC-2000; 2000US-0256418P.
PR	
XX	
XX	(GERO-) GERON CORP.
PA	
XX	
XX	Irving JM, Lebkowski JS;
PI	
XX	
XX	WPI; 2002-723123/78.
DR	
XX	
XX	Novel replication-conditional virus useful for cytolysis of target cells
PT	e.g. cancer cells and preparing a medicament for treating cancer,
PT	comprises heterologous replication element in an adenovirus-based
PT	construct.
XX	
XX	Claim 11; Page 26-29; 32pp; English.
PS	
XX	
XX	The present invention relates to a new replication-conditional virus with
CC	a genome comprising adenovirus replication genes and one or more
CC	heterologous gene(s) that functionally replaces one or more adenovirus
CC	gene(s) required for replication or assembly of the virus. The invention
CC	is useful for killing a cancer cell (such as lung, pancreatic cancer,
CC	medulloblastoma, cervical carcinoma, fibrosarcoma or osteosarcoma),
CC	killing a cell expressing TERT (telomerase reverse transcriptase), and in
CC	preparing a medicament for treating cancer and a condition associated
CC	with increased expression of TERT in affected cells, in a subject. The
CC	invention is also useful for cytolysis of specific target cells. The
CC	invention is further useful for producing replication defective
CC	adenovirus vector which is useful for transient expression of a
CC	heterologous therapeutic gene to correct a congenital defect, introducing
CC	proinflammatory or antiinflammatory activity, enhancing telomerase
CC	function, and delivering heterologous effector genes that induce killing
CC	of the transduced cells. The invention is more safe for use in cancer
CC	therapy. The present nucleic acid sequence represents the human TERT
CC	sequence contained within a lambda clone sequence of the invention
XX	
XX	Sequence 15418 BP; 4518 A; 3797 C; 3765 G; 3338 T; 0 U; 0 Other;
SQ	

Query Match 100.0%; Score 1001; DB 6; Length 15418;
Best Local Similarity 100.0%; Pred. No. 6.4e-291;
Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db	11500	GGCTGGGAAATACAGGCAACCGCCACCATGCCAGCTAAATTTTGTATTTTGTAGTAGAGA	11559
Qy	61	CGGGGGTGGGGGTGGGGTTCACCATGTTGGCCAGGCTGCTCGAACTTCTGCACTCTCAGA	120
Db	11560	CGGGGGTGGGGGTGGGGTTCACCATGTTGGCCAGGCTGCTCGAACTTCTGCACTCTCAGA	11619
Qy	121	TGATTCACCTGCCTCTGCGCTCTCTAAAGTGCTGGGAATACAGGTGTGAGCACCATGCCCA	180
Db	11620	TGATTCACCTGCCTCTGCGCTCTCTAAAGTGCTGGGAATACAGGTGTGAGCACCATGCCCA	11679
Qy	181	GCTCAGAAATTTACTCTGTTTTAGAAAACATCTGGGTCTGAGGTAGGAAGCTCACCCACTCA	240
Db	11680	GCTCAGAAATTTACTCTGTTTTAGAAAACATCTGGGTCTGAGGTAGGAAGCTCACCCACTCA	11739
Qy	241	AGTGTGTGTGTTTTTAAGCCAATGATAGAAATTTTTTATTGTTGTAGAACTCTTTGA	300
Db	11740	AGTGTGTGTGTTTTTAAGCCAATGATAGAAATTTTTTATTGTTGTAGAACTCTTTGA	11799
Qy	301	TGTTTTACACTGTGATGACTAAGACATCATCAGCTTTCAAAGACACACTAATCTGACCC	360
Db	11800	TGTTTTACACTGTGATGACTAAGACATCATCAGCTTTCAAAGACACACTAATCTGACCC	11859
Qy	361	ATAACTCTGGGGTGTCTTCTGGGTATCAGCGATCTTCAATGAATGCGGAGGCGTTTCC	420
Db	11860	ATAACTCTGGGGTGTCTTCTGGGTATCAGCGATCTTCAATGAATGCGGAGGCGTTTCC	11919
Qy	421	TGGCATGCAATGGTGTAAATTTACTTCAGACATAATCTTCTGCTTCCATTTCTCTCTTC	480
Db	11920	TGGCATGCAATGGTGTAAATTTACTTCAGACATAATCTTCTGCTTCCATTTCTCTCTTC	11979
Qy	481	CCTCTTTTAAAAATGTGTGTTTTCTATGCTTGGCTTCTCTGCAGAGAACCACTGTAAGCTACA	540
Db	11980	CCTCTTTTAAAAATGTGTGTTTTCTATGCTTGGCTTCTCTGCAGAGAACCACTGTAAGCTACA	12039
Qy	541	ACTTAACTTTTGTGGAAACAAATTTTCCAAACCGCCCTTTGCCCTAGTGGCAGAGACAA	600
Db	12040	ACTTAACTTTTGTGGAAACAAATTTTCCAAACCGCCCTTTGCCCTAGTGGCAGAGACAA	12099
Qy	601	TTCCAAACACAGCCCTTTAAAAAGCTTAGGGTACACTAAGGGGATTTCTAGAGAGCG	660
Db	12100	TTCCAAACACAGCCCTTTAAAAAGCTTAGGGTACACTAAGGGGATTTCTAGAGAGAGCG	12159
Qy	661	ACCCGTAATCCTTAAGTATTTTACAAGACGAGGCTTAACCTCCAGCAGCGTGAACGCCCAGG	720
Db	12160	ACCCGTAATCCTTAAGTATTTTACAAGACGAGGCTTAACCTCCAGCAGCGTGAACGCCCAGG	12219
Qy	721	GAGGGTCGAGGCGCTGTTCAAATGCTAGCTCCATAATAAAGCAATTTCTCCGGCAGTT	780
Db	12220	GAGGGTCGAGGCGCTGTTCAAATGCTAGCTCCATAATAAAGCAATTTCTCCGGCAGTT	12279
Qy	781	TCTGAAAGTAGGAAAGGTTCATTTAAGGTTCGGTTTGTTAGCATTTCAAGTGTTCGCCGA	840
Db	12280	TCTGAAAGTAGGAAAGGTTCATTTAAGGTTCGGTTTGTTAGCATTTCAAGTGTTCGCCGA	12339
Qy	841	CCTCAGCTACAGCATTCCTGCAAGGCGCTCGGAGACCCAGAAAGTTTCTCGCCCTTAGAT	900
Db	12340	CCTCAGCTACAGCATTCCTGCAAGGCGCTCGGAGACCCAGAAAGTTTCTCGCCCTTAGAT	12399
Qy	901	CCTCAGCTACAGCATTCCTGCAAGGCGCTCGGAGACCCAGAAAGTTTCTCGCCCTTAGAT	960
Db	12400	CCTCAGCTACAGCATTCCTGCAAGGCGCTCGGAGACCCAGAAAGTTTCTCGCCCTTAGAT	12459
Qy	961	GCGGGGGCCCAAGGTCTGGAGGGGACAGGTGGCCGTGTGCGC	1001
Db	12460	GCGGGGGCCCAAGGTCTGGAGGGGACAGGTGGCCGTGTGCGC	12500

RESULT 4
AAL38595
ID AAL3
XX
AC AAL3

[illegible]

16-AUG-2002 (first entry)
DNA of plasmid pGRN144 containing human hTERT gene.

DNA of plasmid pGRN144 containing human hTERT gene.

Homo sapiens.
Unidentified.
Chimeric.

30-MAY-2002.

26-NOV-2001; 2001WO-US044309.

27-NOV-2000; 2000US-0253357P.

27-NOV-2000; 2000US-0253337F.
27-NOV-2000; 2000US-0253443P.

13-FEB-2001; 2001US-00783203.

(GERO-) GERON CORP.

Gold JD, Lebrowski JS;

WPI; 2002-479952/51.

Depleting a cell e.g., human embryonic stem cell population of undifferentiated stem cells (UC) for use in regenerative medicine comprises genetically altering UC in a population to express nucleic acid encoding a lethal product.

Example 9; Page 62-66; 67pp; English.

The invention relates to a system for depleting a cell population of undifferentiated stem cells, by introducing nucleic acids of structure P-X, where X is a nucleic acid encoding product that is lethal to a cell in which it is expressed; or renders a cell in which it is expressed susceptible to the lethal effect of an external agent, and P is a transcriptional control element causing X to be preferentially expressed in the undifferentiated stem cells. The system is used for depleting a cell population (preferably, human embryonic stem cells) of undifferentiated stem cells. A population of differentiated cells is useful in regenerative medicine, and for preparing antibodies and cDNA libraries that are specific for a differentiated phenotype. The cell populations are also useful for drug screening and therapeutic applications. The differentiated cells are useful for tissue reconstruction or regeneration in a human patient in need of treatment. The cells are administered in a manner that permits to graft to the intended tissue side and reconstitute or regenerate the functionally deficient area. The neural progenitor cells are useful for treating acute or chronic damage to the nerve system e.g. epilepsy, stroke, ischaemia, Huntington's disease, Parkinson's disease, multiple sclerosis, leukodystrophies, neuritis, etc. The hepatocytes and hepatocyte precursors are useful for assessing animal models for ability to repair liver damage. The cardiomyocyte population is useful for assessing animal models for cryoinjury, regenerating cardiac muscle and to treat insufficient cardiac function. This polynucleotide sequence represents the DNA of plasmid pGRN144 containing the human hTERT gene relating to the invention.

Sequence 15418 BP; 4519 A; 3797 C; 3764 G; 3338 T; 0 U; 0 Other;

```
Query Match      100.0%; Score 1001; DB 6; Length 15418;
Best Local Similarity 100.0%; Pred. No. 6.4e-291;
Matches 1001: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy 1 GGCTGGGATTACAGGACCCCGCCACCATGCCAGTAAATTTTGTATTTTGTAGTAGAGA 60
Db 11500 GGCTGGGATTACAGGACCCCGCCACCATGCCAGTAAATTTTGTATTTTGTAGTAGAGA 11559
Qy 61 CGGGGGTGGGGTGGGGTTCACCATGTTGGCCAGGCTGGTTCGAACTTCCTGACCTCAGA 120
Db 11560 CGGGGGTGGGGTGGGGTTCACCATGTTGGCCAGGCTGGTTCGAACTTCCTGACCTCAGA 11619
Qy 121 TGATCCACCTGCTCGCTCCTAAAGTGTGCGGATTACAGGTGTGAGCCACCATGCCCA 180
Db 11620 TGATCCACCTGCTCGCTCCTAAAGTGTGCGGATTACAGGTGTGAGCCACCATGCCCA 11679
Qy 181 GCTCAGAAATTTACTCTGTGTTAGAAACATCTCGGCTCTGAGGTGAGGAAGCTCACCCCACTCA 240
Db 11680 GCTCAGAAATTTACTCTGTGTTAGAAACATCTCGGCTCTGAGGTGAGGAAGCTCACCCCACTCA 11739
Qy 241 AGTGTGTGGTGTGTTTAAAGCAATGATAGAAATTTTATTTATTTGTTAGAACACTCTTGA 300
Db 11740 AGTGTGTGGTGTGTTTAAAGCAATGATAGAAATTTTATTTATTTGTTAGAACACTCTTGA 11799
Qy 301 TGTTTACATGCTGATGACTAAGACATCATCAGCTTTTCAAGACACACTAACTGCACCC 360
Db 11800 TGTTTACATGCTGATGACTAAGACATCATCAGCTTTTCAAGACACACTAACTGCACCC 11859
Qy 361 ATAATACCTGGGGTGTCTTCTGGGTATCAGCATCTTCAATGAAATCCGGGAGGGGTTTCC 420
Db 11860 ATAATACCTGGGGTGTCTTCTGGGTATCAGCATCTTCAATGAAATCCGGGAGGGGTTTCC 11919
Qy 421 TCGCCATGACATGGTGTAAATTAATCTCAGCATTAATCTTCTGCTTCCATTTCTTCTTC 480
Db 11920 TCGCCATGACATGGTGTAAATTAATCTCAGCATTAATCTTCTGCTTCCATTTCTTCTTC 11979
Qy 481 CCTCTTTTAAATTTGTTTCTATGTTGGCTTCTCTGCAGAGAACAGTGTAGTACATA 540
Db 11980 CCTCTTTTAAATTTGTTTCTATGTTGGCTTCTCTGCAGAGAACAGTGTAGTACATA 12039
Qy 541 ACTTAACTTTTGTGGAAACAATTTTCCAAACCGCCCTTTCCTAGTGCAGAGACAA 600
Db 12040 ACTTAACTTTTGTGGAAACAATTTTCCAAACCGCCCTTTCCTAGTGCAGAGACAA 12099
Qy 601 TTCAAAACACAGCCCTTTTAAAAAGGCTTAGGGATCACTAAGGGGATTTCTAGAGAGCG 660
Db 12100 TTCAAAACACAGCCCTTTTAAAAAGGCTTAGGGATCACTAAGGGGATTTCTAGAGAGCG 12159
Qy 661 ACCGTAACTCTAGTATTTACAGACAGAGCTTAACCTCAGCGAGGTGACAGCCACGG 720
Db 12160 ACCGTAACTCTAGTATTTACAGACAGAGCTTAACCTCAGCGAGGTGACAGCCACGG 12219
Qy 721 GAGGTGCGAGGCTGTTCAATGCTAGCTCCATAAATAAAGCAATTTCTCCGCGAGTT 780
Db 12220 GAGGTGCGAGGCTGTTCAATGCTAGCTCCATAAATAAAGCAATTTCTCCGCGAGTT 12279
Qy 781 TCTGAAGTAGGAAGGTTTACATTTAAGTTGCGTTTGGTTAGTACATTTCAAGTTTGGCGA 840
Db 12280 TCTGAAGTAGGAAGGTTTACATTTAAGTTGCGTTTGGTTAGTACATTTCAAGTTTGGCGA 12339
Qy 841 CCTGAGCTACAGCATCCCTGACAGGCTTCGGAGACCCAGAGTTTCTCGCCCTTAGAT 900
Db 12340 CCTGAGCTACAGCATCCCTGACAGGCTTCGGAGACCCAGAGTTTCTCGCCCTTAGAT 12399
Qy 901 CCAACTTGACCAACCCGAGTCTGGATTCTCTGGGAAGTCTCAGCTCTCTCGGGTTGT 960
Db 12400 CCAACTTGACCAACCCGAGTCTGGATTCTCTGGGAAGTCTCAGCTCTCTCGGGTTGT 12459
Qy 961 GCCGGGGCCCGAGTCTCGAGGGGACCAAGTGGCCGTGGC 1001
Db 12460 GCCGGGGCCCGAGTCTCGAGGGGACCAAGTGGCCGTGGC 12500

RESULT 5
ADC21253
ID ADC21253 standard; DNA; 15418 BP.

XX ADC21253;
XX 18-DEC-2003 (first entry)
XX Lambda clone (lambdaGph15) containing human TERT DNA.
XX Viral vector; heterologous control element; gene expression;
XX human telomerase reverse transcriptase; hTERT; tumour specific gene;
XX cell death; transcriptional control element; cancer cell;
XX human telomerase RNA component; hTR; cancer cell; liver cancer;
XX prostate cancer; muscle cancer; neural cell cancer; lung cancer;
XX pancreatic cancer; medulloblastoma; cervical carcinoma; fibrosarcoma;
XX osteosarcoma; lambda clone; lambdaGph15; human; ds.
XX Synthetic.
XX Homo sapiens.
XX Bacteriophage lambda.
XX US2003099616-A1.
XX 29-MAY-2003.
XX 25-JUL-2002; 2002US-00206447.
XX 25-JUL-2001; 2001US-0308029P.
XX (IRVI/) IRVING J M.
XX (KARP/) KARP D B.
XX (SCHI/) SCHIFF J M.
XX Irving JM, Karpf DB, Schiff JM;
XX WPI; 2003-730140/69.
XX New dual specificity vectors driven by the telomerase promoter, useful
XX for killing or slowing the growth of tumor cells, or for treating cancer,
XX e.g. liver cancer, prostate cancer, lung cancer, or pancreatic cancer.
XX Example 1; Page 13-20; 25pp; English.
XX The present invention relates to a viral vector comprising first and
XX second genes controlled by heterologous control elements, where the first
XX gene is preferentially expressed in cells expressing human telomerase
XX reverse transcriptase (hTERT), and another gene under the control of a
XX heterologous transcriptional control element for a tissue or tumour
XX specific gene other than TERT, and where transduction of the vector into
XX a mammalian cell expressing TERT causes the death of the cell or its
XX progeny. In particular, the second gene may be under the control of a
XX transcriptional control element for a tissue specific gene selected from
XX albumin, alpha-fetoprotein, prostate-specific antigen, mitochondrial
XX creatine kinase, myelin basic protein, glial fibrillary acidic protein,
XX and neuron-specific enolase. The second gene may be under the control of
XX a transcriptional control element for a human telomerase RNA component
XX (hTR). The vector of the invention is useful for killing a cancer cell,
XX or treating a subject for a condition associated with increased
XX expression of TERT in affected cells. The vector is also useful in the
XX preparation of a medicament for treatment of a condition associated with
XX increased expression of TERT, particularly cancer, and especially liver
XX cancer, prostate cancer, muscle cancer, neural cell cancer, lung cancer,
XX pancreatic cancer, medulloblastoma, cervical carcinoma, fibrosarcoma, and
XX osteosarcoma. The present sequence represents a lambda clone
XX (lambdaGph15) containing human TERT DNA.
XX Sequence 15418 BP; 4518 A; 3797 C; 3765 G; 3338 T; 0 U; 0 Other;
XX Query Match 100.0%; Score 1001; DB 10; Length 15418;
XX Best Local Similarity 100.0%; Pred. No. 6.4e-291;
XX Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGCTGGGATTACAGGACCCCGCCACCATGCCAGTAAATTTTGTATTTTGTAGTAGAGA 60
Db 11500 GGCTGGGATTACAGGACCCCGCCACCATGCCAGTAAATTTTGTATTTTGTAGTAGAGA 11559

```
Qy 61 CGGGGTGGGGTGGGGTTCACCATGTTGGCCAGGCTGTCTCGAACTTCTGACCTCAGA 120
Db 11560 CGGGGTGGGGTGGGGTTCACCATGTTGGCCAGGCTGTCTCGAACTTCTGACCTCAGA 11619
Qy 121 TGATCCACCTGCTCTGCTCTCCCTCTAAAGTGTGGGATTCACAGGTGTGAGCCACCATGCCCCA 180
Db 11620 TGATCCACCTGCTCTGCTCTCCCTCTAAAGTGTGGGATTCACAGGTGTGAGCCACCATGCCCCA 11679
Qy 181 GCTCAGAAATTTACTCTGTTTAGAAAACATCTGGGTCTGAGGTAGGAAGCTCACCCCACTCA 240
Db 11680 GCTCAGAAATTTACTCTGTTTAGAAAACATCTGGGTCTGAGGTAGGAAGCTCACCCCACTCA 11739
Qy 241 AGTGTGTGTGTGTTTAAAGCCATGATAGAAATTTTATTTTATTTGTTTGTAGAACACTCTTGA 300
Db 11740 AGTGTGTGTGTGTTTAAAGCCATGATAGAAATTTTATTTTATTTGTTTGTAGAACACTCTTGA 11799
Qy 301 TGTTTTACACTGTGATGACTAAGACATCATCAGCTTTTCAAAGACACACTAACTGACACCC 360
Db 11800 TGTTTTACACTGTGATGACTAAGACATCATCAGCTTTTCAAAGACACACTAACTGACACCC 11859
Qy 361 ATAATACCTGGGTGTCTTCTGGGTATCAGCGATCTTCATTTGAATGCGGAGGCGTTTCC 420
Db 11860 ATAATACCTGGGTGTCTTCTGGGTATCAGCGATCTTCATTTGAATGCGGAGGCGTTTCC 11919
Qy 421 TCGGCATGACATGGTGTGTTAACTTACTCCAGCATATCTTCTGCTTCCATTTCTCTCTTC 480
Db 11920 TCGGCATGACATGGTGTGTTAACTTACTCCAGCATATCTTCTGCTTCCATTTCTCTCTTC 11979
Qy 481 CCTCTTTTAAATATGTTTCTATGTTGGCTTCTGCGAGAGAACAGTGAAGTGAAGTAC 540
Db 11980 CCTCTTTTAAATATGTTTCTATGTTGGCTTCTGCGAGAGAACAGTGAAGTGAAGTAC 12039
Qy 541 ACTTAACTTTGTTGGAAACAAATTTTCCAAACCGCCCTTTGGCTTGTGCTAGTGCGCAGACAA 600
Db 12040 ACTTAACTTTGTTGGAAACAAATTTTCCAAACCGCCCTTTGGCTTGTGCTAGTGCGCAGACAA 12099
Qy 601 TTCAAAACACAGCCCTTTAAAGGCTTAGGATCACTAAGGGATTTCTAGNAGAGCG 660
Db 12100 TTCAAAACACAGCCCTTTAAAGGCTTAGGATCACTAAGGGATTTCTAGNAGAGCG 12159
Qy 661 ACCGTAATCTTAGTATTTACAGAGCAGGCTAACTTCCAGCGAGGCTGACAGCCGAGG 720
Db 12160 ACCGTAATCTTAGTATTTACAGAGCAGGCTAACTTCCAGCGAGGCTGACAGCCGAGG 12219
Qy 721 GAGGTCGAGGCTGTTCAAATGCTAGCTCCATAAATAAGCAATTTCTCCGGCAGTT 780
Db 12220 GAGGTCGAGGCTGTTCAAATGCTAGCTCCATAAATAAGCAATTTCTCCGGCAGTT 12279
Qy 781 TCTGAAAGTAGGAAGGTTACATTTAAGGTTGCGTTTGTAGCAATTTCACTGTTTGC 840
Db 12280 TCTGAAAGTAGGAAGGTTACATTTAAGGTTGCGTTTGTAGCAATTTCACTGTTTGC 12339
Qy 841 CCTCAGCTACAGCATCCCTGCAAGGCTCGGGAGACCCAGAGTTTCTCGCCCTTAGAT 900
Db 12340 CCTCAGCTACAGCATCCCTGCAAGGCTCGGGAGACCCAGAGTTTCTCGCCCTTAGAT 12399
Qy 901 CCAACTTTGAGCAACCGGAGTCTGGATTCCTGGGAAGTCTCTCAGCTGTCTCGGGTGT 960
Db 12400 CCAACTTTGAGCAACCGGAGTCTGGATTCCTGGGAAGTCTCTCAGCTGTCTCGGGTGT 12459
Qy 961 GCCGGGGCCCGAGTCTGGAGGGACCAAGTGGCGGTGGC 1001
Db 12460 GCCGGGGCCCGAGTCTGGAGGGACCAAGTGGCGGTGGC 12500
```

RESULT 6

AAH41091

ID AAH41091 standard; DNA; 3962 BP.

XX

AC AAH41091;

XX

DT 29-AUG-2001 (first entry)

```
XX Telomerase reverse transcriptase (TERT) DNA.
DE Phenotype switch molecule; phenotype-related gene battery;
KW gene localisation; telomere reverse transcriptase; TERT; ds.
XX Unidentified.
OS WO200138515-A1.
PN 31-MAY-2001.
XX 17-NOV-2000; 2000WO-CN000427.
XX 19-NOV-1999; 99CN-00121466.
XX (BIAN/) BIAN X.
PI Bian X;
XX WPI; 2001-367684/38.
DR Isolating phenotype switch molecules and phenotype-related gene batteries
XX from complex genomes of higher animals and plants, useful e.g. in gene
XX localization and classification analysis.
XX Example 7; Page 27-29; 35pp; Chinese.
XX This invention relates to a method for isolating phenotype switch
XX molecules and phenotype-related gene batteries from complex genomes of
XX higher animals and plants. The method is useful in gene localisation and
XX classification analysis, studying gene development networks and function
XX networks, and designing drugs based on regulatory sequences of the
XX phenotypes for disease treatment. The present sequence represents DNA
XX encoding a telomere reverse transcriptase (TERT), which is used in an
XX example illustrating the use of the method of the invention
SQ Sequence 3962 BP; 782 A; 1157 C; 1113 G; 910 T; 0 U; 0 Other;
Query Match 98.8%; Score 989; DB 4; Length 3962;
Best Local Similarity 99.9%; Pred. No. 1.4e-287;
Matches 1000; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Qy 1 GCGTGGGATTCACAGGCACCGCCACCATGCGCCAGCTAAATTTTGTATTTTGTAGTACAGA 60
Db 1882 GCGTGGGATTCACAGGCACCGCCACCATGCGCCAGCTAAATTTTGTATTTTGTAGTACAGA 1941
Qy 61 CGGGGGTGGGGGTGGGGTTCACCATGTTGGCCAGGCTGTCTCGAACTTCTGACCTCAGA 120
Db 1942 CGGGGGTGGGGGTGGGGTTCACCATGTTGGCCAGGCTGTCTCGAACTTCTGACCTCAGA 2001
Qy 121 TGATCCACCTGCTCTGCTCTCCCTCTAAAGTGTGTGGGATTCACAGGTGTGAGCCACCATGCCCCA 180
Db 2002 TGATCCACCTGCTCTGCTCTCCCTCTAAAGTGTGTGGGATTCACAGGTGTGAGCCACCATGCCCCA 2061
Qy 181 GCTCAGAAATTTACTCTGTTTAGAAAACATCTGGGTCTGAGGTAGGAAGCTCACCCCACTCA 240
Db 2062 GCTCAGAAATTTACTCTGTTT- GAAACATCTGGGTCTGAGGTAGGAAGCTCACCCCACTCA 2120
Qy 241 AGTGTGTGTGTGTTTAAAGCCATGATAGAAATTTTATTTTATTTGTTTGTAGAACACTCTTGA 300
Db 2121 AGTGTGTGTGTGTTTAAAGCCATGATAGAAATTTTATTTTATTTGTTTGTAGAACACTCTTGA 2180
Qy 301 TGTTTTACACTGTGATGACTAAGACATCATCAGCTTTTCAAAGACACACTAACTGACACCC 360
Db 2181 TGTTTTACACTGTGATGACTAAGACATCATCAGCTTTTCAAAGACACACTAACTGACACCC 2240
Qy 361 ATAATACCTGGGTGTCTTCTGGGTATCAGCGATCTTCATTTGAATGCGGAGGCGTTTCC 420
Db 2241 ATAATACCTGGGTGTCTTCTGGGTATCAGCGATCTTCATTTGAATGCGGAGGCGTTTCC 2300
Qy 421 TCGGCATGACATGGTGTGTTAACTTACTCCAGCATATCTTCTGCTTCCATTTCTCTCTTC 480
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QY 181 GCTCAGAAATTAATCTCTGTTTAGAACATCTGGGCTGAGGTAGGAGCTCACCCCACTCA 240
DB 2133 GCTCAGAAATTAATCTCTGTTT-GAAACATCTGGGCTGAGGTAGGAGCTCACCCCACTCA 2191
QY 241 AGTGTGTGCTGTTTAAAGCAATGATAGAAATTTTATTTTATTTGTTAGAACACTCTTTGA 300
DB 2192 AGTGTGTGCTGTTTAAAGCAATGATAGAAATTTTATTTTATTTGTTAGAACACTCTTTGA 2251
QY 301 TGTTTTACATCTGATGACTAAGACATCATCAGCTTTTCAAAGACACACTAACTGCACCC 360
DB 2252 TGTTTTACATCTGATGACTAAGACATCATCAGCTTTTCAAAGACACACTAACTGCACCC 2311
QY 361 ATAATACCTGGGCTCTCTCTGGGTATCAGGATCTTCAATGAATCCGGGAGGGTTTCC 420
DB 2312 ATAATACCTGGGCTCTCTCTGGGTATCAGGATCTTCAATGAATCCGGGAGGGTTTCC 2371
QY 421 TCGCCATGCATGGTGTAAATTAATCTCAGCATAACTCTCTGCTTCCATTTCTTCTTTC 480
DB 2372 TCGCCATGCATGGTGTAAATTAATCTCAGCATAACTCTCTGCTTCCATTTCTTCTTTC 2431
QY 481 CCTCTTTTAAATTTGTTTCTATGTTGGCTTCTCTGCAGAGAACCAAGTGAAGCTACA 540
DB 2432 CCTCTTTTAAATTTGTTTCTATGTTGGCTTCTCTGCAGAGAACCAAGTGAAGCTACA 2491
QY 541 ACTTAACCTTTGTTGGAAACAAATTTCCAAACCGCCCTTTGCCCTAGTGCAGAGACAA 600
DB 2492 ACTTAACCTTTGTTGGAAACAAATTTCCAAACCGCCCTTTGCCCTAGTGCAGAGACAA 2551
QY 601 TTCACAAACACAGCCCTTTTAAAGGCTTAGGGATCACTAAGGGGATTTCTAGAAGAGCG 660
DB 2552 TTCACAAACACAGCCCTTTTAAAGGCTTAGGGATCACTAAGGGGATTTCTAGAAGAGCG 2611
QY 661 ACCGTAATCCTAAGTATTACAAGACAGGCTAACTCCAGCGAGGCTGACAGCCGAG 720
DB 2612 ACCGTAATCCTAAGTATTACAAGACAGGCTAACTCCAGCGAGGCTGACAGCCGAG 2671
QY 721 GAGGTCGAGGCTGTCAATGCTAGCTCCATTAATTAAGCAATTTCTCCGGCAGTT 780
DB 2672 GAGGTCGAGGCTGTCAATGCTAGCTCCATTAATTAAGCAATTTCTCCGGCAGTT 2731
QY 781 TCTGAAGTATGAGAAAGGTATACATTTAAGTTTGGTTTGTAGCATTTTCAAGTTTGGCGA 840
DB 2732 TCTGAAGTATGAGAAAGGTATACATTTAAGTTTGGTTTGTAGCATTTTCAAGTTTGGCGA 2791
QY 841 CCTCAGCTACAGCATCCCTCGAAGGCTCTCGGAGACCCAGAAAGTTTCTCGCCCTTAGAT 900
DB 2792 CCTCAGCTACAGCATCCCTCGAAGGCTCTCGGAGACCCAGAAAGTTTCTCGCCCTTAGAT 2851
QY 901 CCAAACTTGAGCAACCCGAGTCTGGATTCTTGGGAAGTCTCAGCTGTCTCGGGTTGT 960
DB 2852 CCAAACTTGAGCAACCCGAGTCTGGATTCTTGGGAAGTCTCAGCTGTCTCGGGTTGT 2911
QY 961 GCCGGGGCCCCAGGCTCTGGAGGGGACCCAGTGGCCGTGTGGC 1001
DB 2912 GCCGGGGCCCCAGGCTCTGGAGGGGACCCAGTGGCCGTGTGGC 2952
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RESULT 8

ADV23865

ID ADV23865 standard; DNA; 4293 BP.

AC ADV23865;

XX 24-FEB-2005 (first entry)

XX Human hTERT gene 5' flanking region, intron 1 and exon 1, SEQ ID 1.

XX Cytostatic; Gene therapy; cancer; telomerase;

XX telomerase reverse transcriptase; hTERT; enzyme; gene; ds.

XX Homo sapiens.

XX US2004248246-A1.

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Key Location/Qualifiers
misc_feature 1..3955
/feature= a
/feature= "This region is specifically claimed in Claims 4
and 15"
misc_feature 2251..3920
/feature= b
/feature= "This region is specifically claimed in Claims 4
and 15"
misc_feature 2791..3955
/feature= c
/feature= "This region is specifically claimed in Claims 4
and 15"
misc_feature 2967..3955
/feature= d
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and 15"
misc_feature 3531..3955
/feature= e
/feature= "This region is specifically claimed in Claims 4
and 15"
misc_feature 3545..3609
/feature= f
/feature= "This region is identical to the Hepatitis B virus
(HBV) integration site in the huH-4 cell line"
misc_feature 3612..3955
/feature= g
/feature= "This region is specifically claimed in Claims 4
and 15"
misc_feature 3661..3955
/feature= h
/feature= "This region is specifically claimed in Claims 4
and 15"
misc_feature 3705..3955
/feature= i
/feature= "This region is specifically claimed in Claims 4
and 15"
misc_feature 3708..3766
/feature= j
/feature= "This region is responsible for full promoter
activity"
misc_feature 3729..3734
/feature= k
/feature= "Upstream E-box"
misc_feature 3828..3955
/feature= l
/feature= "This region is specifically claimed in Claims 4
and 15"
misc_feature 3883..3955
/feature= m
/feature= "This region is specifically claimed in Claims 4,
15, 19 and 20"
5'UTR 3916..3970
/feature= n
misc_feature 3937..3942
/feature= o
/feature= "Downstream E-box"
CDS 3971..4189
/feature= p
/feature= "partial
/product= "hTERT exon 1 protein"
exon 3971..4189
/feature= q
/feature= "number= 1
/feature= r
primer_bind 4029..4050
/feature= r
/feature= "Binding site for GW2 primer (SEQ ID 4)"
intron 4190..4293
/feature= s
/feature= "number= 1
```


PD 09-DEC-2004.
XX
XX
XX 05-JUN-2003; 2003US-00456830.
XX
XX 05-JUN-2003; 2003US-00456830.
XX (USAS) NASA US NAT AERO & SPACE ADMIN.
XX
XX Horikawa I, Barrett JC;
XX
XX WPI, 2005-020562/02.
XX P-PSDB; ADV23866.
XX
XX New regulatory control sequence comprising a promoter that directs
XX differential expression of an operably linked heterologous nucleic acid
XX sequence in a first cell type, useful for preparing a composition for
XX treating cancer.
XX
XX Claim 4; SEQ ID NO 1; 46pp; English.
XX
XX The present invention relates to a new regulatory control sequence (I)
XX which is useful for preparing a composition for treating cancer. (I)
XX comprises: (a) a promoter that directs differential expression of an
XX operably linked heterologous nucleic acid sequence (e.g. cytotoxins) in a
XX first cell type as compared to a second cell type, where the first cell
XX type is a telomerase-positive or a cancer cell and the second cell type
XX is a telomerase-negative or a normal somatic cell; and (b) at least one
XX exogenous E-box element linked in cis with the promoter sequence and that
XX enhances the differential expression directed by the promoter. The
XX promoter is preferably an human telomerase reverse transcriptase (hTERT)
XX promoter. hTERT is the catalytic subunit of the human telomerase complex,
XX which is responsible for the replication of telomeres. E-box elements are
XX regulatory control elements that are recognized by numerous transcription
XX factors, e.g. transcription factors from the basic helix-loop-helix
XX structural family. Differential E-box-mediated repression of hTERT gene
XX promoter activity has been discovered, where repression occurs in normal
XX cells but not in many cancer cells. By linking E-box elements in cis with
XX TERT transcriptional regulatory sequences, the expression of heterologous
XX sequences operably linked to the TERT transcriptional regulatory
XX sequences, can be preferentially suppressed in normal cells. However, the
XX expression of such heterologous sequences is not suppressed in cancer
XX cells. The present sequence is the nucleotide sequence in the 5'-flanking
XX region, exon 1 and intron 1 of the hTERT gene, used to illustrate the
XX invention.
XX
XX Sequence 4293 BP; 817 A; 1278 C; 1234 G; 961 T; 0 U; 3 Other;

Query Match 98.8%; Score 988.6; DB 14; Length 4293;
Best Local Similarity 99.8%; Pred. No. 1.9e-287;
Matches 999; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
QY 1 GCCTGGGATTACAGGCACCGGCACATGCCAGCTAATTTTGTATTTTAGTAGAGA 60
DB 1927 GCCTGGGATTACAGGCACCGGCACATGCCAGCTAATTTTGTATTTTAGTAGAGA 1986
QY 61 CGGGGGTGGGGTGGGGTTCACATGTTGGCCAGCTGTCGAACTTCTGACCTCAGA 120
DB 1987 CGGGGGTGGGGTGGGGTTCACATGTTGGCCAGCTGTCGAACTTCTGACCTCAGA 2046
QY 121 TGATCCACTGCTCTGCTCTCCTAAAGTCTGGGATTACAGGTGTGAGCCACCATGCCA 180
DB 2047 TGATCCACTGCTCTGCTCTCCTAAAGTCTGGGATTACAGGTGTGAGCCACCATGCCA 2106
QY 181 GCTCAGAAATTTACTCTGTTTAGAAAACATCTGGGTCTGAGGTAGGAAGCTCACCCACTCA 240
DB 2107 GCTCAGAAATTTACTCTGTTT-GAAACATCTGGGTCTGAGGTAGGAAGCTCACCCACTCA 2165
QY 241 AGTGTGTGGTGTGTTTAGCCCAATGATAGAAATTTTATTTTCTGTAGACACTCTGA 300
DB 2166 AGTGTGTGGTGTGTTTAGCCCAATGATAGAAATTTTATTTTCTGTGTAGAACTCTGA 2225
QY 301 TGTTTTACACTGTGATGACTAGACATCATCAGCTTTTCAAAGACACACTAATCTGACCC 360

DB 2226 TGTTTTACACTGTGATGACTAGACATCATCAGCTTTTCAAAGACACACTAATCTGACCC 2285
QY 361 ATAATACTGGGGTGTCTTCTGGGTATCAGCGATCTTCAATGAAATGCCGGGAGGCGTTTCC 420
DB 2286 ATAATACTGGGGTGTCTTCTGGGTATCAGCGATCTTCAATGAAATGCCGGGAGGCGTTTCC 2345
QY 421 TCGCCATGCAATGGTGTAAATTAATCTCAGCATAAATCTTCTGCTTCAATTTCTTCTTTC 480
DB 2346 TCGCCATGCAATGGTGTAAATTAATCTCAGCATAAATCTTCTGCTTCAATTTCTTCTTTC 2405
QY 481 CCTCTTTTAAATTTGGTGTCTTCTATGTGGCTTCTCTGCAGAGAACCACTGTAAGCTACA 540
DB 2406 CCTCTTTTAAATTTGGTGTCTTCTATGTGGCTTCTCTGCAGAGAACCACTGTAAGCTACA 2465
QY 541 ACTTAACTTTTGGTGTAAATTTTCAAACCGCCCTTTGGCCCTAGTGGCAGACACAA 600
DB 2466 ACTTAACTTTTGGTGTAAATTTTCAAACCGCCCTTTGGCCCTAGTGGCAGACACAA 2525
QY 601 TTCAAAACACAGCCCTTTTAAAGGCTTAAAGGATCACTAAGGGGATTTCTAGAAAGCGG 660
DB 2526 TTCAAAACACAGCCCTTTTAAAGGCTTAAAGGATCACTAAGGGGATTTCTAGAAAGCGG 2585
QY 661 ACCGTTAATCTTAAATTTTCAAGAGCAGGCTTAACCTCCAGCGGCGTGCAGCCCGAGG 720
DB 2586 ACCGTTAATCTTAAATTTTCAAGAGCAGGCTTAACCTCCAGCGGCGTGCAGCCCGAGG 2645
QY 721 GAGGGTGGCGGCTTGTTCAAATGCTAGCTCCATAAATAAAGCAATTTCTCCGCGAGTT 780
DB 2646 GAGGGTGGCGGCTTGTTCAAATGCTAGCTCCATAAATAAAGCAATTTCTCCGCGAGTT 2705
QY 781 TCTGAAAGTAGGAAAGGTTACATTTAAGGTTGCGTTTGTAGCATTTTCAGTGTTCGCCGA 840
DB 2706 TCTGAAAGTAGGAAAGGTTACATTTAAGGTTGCGTTTGTAGCATTTTCAGTGTTCGCCGA 2765
QY 841 CCTCAGCTACAGCATCCTTCAGGCTTCGCGAGACCCAGAAAGTTTCTCGCCCTTAGAT 900
DB 2766 CCTCAGCTACAGCATCCTTCAGGCTTCGCGAGACCCAGAAAGTTTCTCGCCCTTAGAT 2825
QY 901 CCAAACTTGACAAACCCGAGTCTGGATTCTCTGGGAGTCTCTCAGCTGTCTGCGGTTGT 960
DB 2826 CCAAACTTGACAAACCCGAGTCTGGATTCTCTGGGAGTCTCTCAGCTGTCTGCGGTTGT 2885
QY 961 GCCGGGGGCCAGGCTGTGGAGGGGACCAAGTGGCCGCTGTGGC 1001
DB 2886 GCCGGGGGCCAGGCTGTGGAGGGGACCAAGTGGCCGCTGTGGC 2926

RESULT 9
ADU82631
ID ADU82631 standard; DNA; 5491 BP.
XX
AC ADU82631;
XX
DT 10-FEB-2005 (first entry)
XX
XX Human hTERT gene nucleotide sequence.
DE
XX
KW Gene expression; transcription; TERT; telomerase reverse transcriptase;
KW cancer therapy; cytostatic; CNS; respiratory; anti-HIV; antineoplastic;
KW antiskilling; hemostatic; antidiabetic; cardiac; antinflammatory;
KW antirheumatic; antithrombotic; neuroprotective; antiasthmatic; vasotropic;
KW gene therapy; apoptosis stimulator; cancer; gene; ds.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 3415..3633
XX FT /*tag= a
XX FT /product= "telomerase reverse transcriptase fragment"
XX FT /partial
XX
XX WO2004099377-A2.

XX DE DNA encoding human telomerase reverse transcriptase (TERT) #1.
XX XX
KW Telomerase reverse transcriptase; TERT; cyrostatic; apoptosis;
KW cell growth inhibitor; antisense oligonucleotide; antisense technology;
KW ds.
XX OS Homo sapiens.
XX XX
FH Key Location/Qualifiers
FT exon 1. .11492
FT /*tag= a
FT /number= 1
FT 11274. .47813
FT /*tag= b
FT /product= "TERT"
FT /note= "Telomerase reverse transcriptase"
FT 11493. .11596
FT /*tag= c
FT /number= 1
FT 11597. .12950
FT /*tag= d
FT /number= 2
FT 12951. .21566
FT /*tag= e
FT /number= 2
FT 21567. .21762
FT /*tag= f
FT /number= 3
FT 21763. .23851
FT /*tag= g
FT /number= 3
FT 23852. .24032
FT /*tag= h
FT /number= 4
FT 24033. .24719
FT /*tag= i
FT /number= 4
FT 24720. .24899
FT /*tag= j
FT /number= 5
FT 24900. .25393
FT /*tag= k
FT /number= 5
FT 25394. .25549
FT /*tag= l
FT /number= 6
FT 25550. .30195
FT /*tag= m
FT /number= 6
FT 30196. .30292
FT /*tag= n
FT /number= 7
FT 30293. .31272
FT /*tag= o
FT /number= 7
FT 31273. .31358
FT /*tag= p
FT /number= 8
FT 31359. .33843
FT /*tag= q
FT /number= 8
FT 33844. .33957
FT /*tag= r
FT /number= 9
FT 33958. .35941
FT /*tag= s
FT /number= 9
FT 35942. .36013
FT /*tag= t
FT /number= 10
FT 36014. .37884
FT /*tag= u

FT exon /number= 10
FT 37885. .38073
FT /*tag= v
FT /number= 11
FT 38074. .41874
FT /*tag= w
FT /number= 11
FT 41875. .42001
FT /*tag= x
FT /number= 12
FT 42002. .42881
FT /*tag= y
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FT 42882. .42943
FT /*tag= z
FT /number= 13
FT 42944. .46129
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FT /number= 13
FT 46130. .46254
FT /*tag= ab
FT /number= 14
FT 46255. .47035
FT /*tag= ac
FT /number= 14
FT 47036. .47173
FT /*tag= ad
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FT /number= 15
FT 47710. .50544
FT /*tag= af
FT /number= 16
XX WO200188198-A1.
XX PN 22-NOV-2001.
XX PD 15-MAY-2001; 2001WO-US015774.
XX PF 16-MAY-2000; 2000US-00572423.
XX PR 07-DEC-2000; 2000US-00733294.
XX PA (ISIS-) ISIS PHARM INC.
XX FI Monia BP, Gaarde WA, Freier SM, Wancewicz E;
XX DR WPI; 2002-075321/10.
XX DR P-PSDB; AAU72735.
XX New compound targeted to nucleic acid molecule encoding telomerase
FT transcriptase (TERT), which specifically hybridizes with and inhibits
FT expression of TERT, useful for modulating apoptosis and inhibiting cell
FT growth.
XX Example 19; Page 112-138; 154pp; English.
PS The invention describes a compound, 8-50 nucleobases in length targeted
XX to a nucleic acid molecule encoding human TERT (telomerase reverse
CC transcriptase), where the compound specifically hybridizes with and
CC inhibits the expression of TERT. A series of oligonucleotides were
CC designed to target different regions of a central gap region consisting of
CC nucleotides in length and composed of a central gap region consisting of
CC ten 2'-deoxynucleotides, flanked on both sides (5' and 3' directions) by
CC five-nucleotide wings. The wings were composed of 2'-methoxyethyl (2'-
CC MOE) nucleotides. The compounds were analysed for their effect on human
CC TERT mRNA levels by reverse transcriptase (RT)-polymerase chain reaction
CC (PCR). The compound is useful for inhibiting the expression of TERT in
CC cells or tissues, for treating a human having disease or condition
CC associated with TERT, for modulating apoptosis, for inhibiting cell
CC growth (preferably, cancer cell growth), in antisense therapy and for
CC diagnostics and therapeutics. This sequence encodes human telomerase

CC reverse transcriptase (TERT) #1, and is used to create antisense
CC oligonucleotides which modify TERT expression, described in the method of
CC the invention

XX Sequence 5152 BP; 10709 A; 13313 C; 15370 G; 12158 T; 0 U; 2 Other;

Query Match 97.2%; Score 972.8; DB 6; Length 5152;
Best Local Similarity 99.5%; Pred. No. 3.9e-282;
Matches 997; Conservative 0; Mismatches 2; Indels 3; Gaps 2;

Qy 1 GGCTGGGATTACAGGACACCGCCACCATGCGCAGCTAATTTTGTATTTTGTAGTAGAGA 60
Db 9230 GGCTGGGATTACAGGACACCGCCACCATGCGCAGCTAATTTTGTATTTTGTAGTAGAGA 9289
Qy 61 CGGGGGTGGGGTGGGGTTCACCATGTGGCCAGGCTGCTCGAATTTCTGACCTCAGA 120
Db 9290 CGGGGGT--GGGTGGGGTTCACCATGTGGCCAGGCTGGTCTCGAATTTCTGACCTCAGA 9347
Qy 121 TGATCCACCTGCGCTCTGCCCTCTAAAGTGTGGGATTCACAGGTGTGAGCCACCATGCCCA 180
Db 9348 TGATCCACCTGCGCTCTGCCCTCTAAAGTGTGGGATTCAGGTGTGAGCCACCATGCCCA 9407
Qy 181 GCTCAGAAATTACTCTGTTTAGAAACATCTGGGTCTGAGGTAGGAAGCTCACCCCACTCA 240
Db 9408 GCTCAGAAATTACTCTGTTTAGAAACATCTGGGTCTGAGGTAGGAAGCTCACCCCACTCA 9467
Qy 241 AGTGTCTGGGTGTTTAAAGCCATGATAGATTTTATTTTATTTTGTAGTACACTCTTGA 300
Db 9468 AGTGTCTGGGTGTTTAAAGCCATGATAGATTTTATTTTATTTTGTAGTACACTCTTGA 9527
Qy 301 TGTTTTACATGTCATGACATAAGACATCATCAGCTTTTCAAAGACACACTAACTGCACCC 360
Db 9528 TGTTTTACATGTCATGACATAAGACATCATCAGCTTTTCAAAGACACACTAACTGCACCC 9587
Qy 361 ATAATCTGGGGTCTCTCTGGGTATCAGGATCTTCATTAATGCGGGAGGGTTTCC 420
Db 9588 ATAATCTGGGGTCTCTCTGGGTATCAGGATCTTCATTAATGCGGGAGGGTTTCC 9647
Qy 421 TCGCATGACATGGTGTAAATTAATCTCAGCATTAATCTCTGCTTCCATTTCTCTCTTC 480
Db 9648 TCGCATGACATGGTGTAAATTAATCTCAGCATTAATCTCTGCTTCCATTTCTCTCTTC 9707
Qy 481 CCTCTTTTAAATTTGTTTCTATGTTGGTCTCTCTGACAGAACAGTGTAGTACATA 540
Db 9708 CCTCTTTTAAATTTGTTTCTATGTTGGTCTCTCTGACAGAACAGTGTAGTACATA 9767
Qy 541 ACTTAACTTTTGTGGACAAATTTTCCAAACCGCCCTTTGCCCTAGTGCAGAGACAA 600
Db 9768 ACTTAACTTTTGTGGACAAATTTTCCAAACCGCCCTTTGCCCTAGTGCAGAGACAA 9827
Qy 601 TTCAAAACACAGCCCTTTAAAGGCTTAGGATCACTAAGGGATTTCTAGAGAGCG 660
Db 9828 TTCAAAACACAGCCCTTTAAAGGCTTAGGATCACTAAGGGATTTCTAGAGAGCG 9887
Qy 661 ACCGTAATCTTAAGTATTTTCAAGACAGGCTTAACCTCCAGCGAGGTGACGCCCAGG 720
Db 9888 ACCGTAATCTTAAGTATTTTCAAGACAGGCTTAACCTCCAGCGAGGTGACGCCCAGG 9947
Qy 721 GAGGGTCGAGGCCCTGTTTCAAATGCTAGCTCCATAAATAAGCAATTTTCTCCGGCAGTT 780
Db 9948 GAGGGTCGAGGCCCTGTTTCAAATGCTAGCTCCATAAATAAGCAATTTTCTCCGGCAGTT 10007
Qy 781 TCTGAAAGTAGAAAGGTTTACATTTAAGTTGCGTTTGTAGCATTTTCAGTGTTCGCGA 840
Db 10008 TCTGAAAGTAGAAAGGTTTACATTTAAGTTGCGTTTGTAGCATTTTCAGTGTTCGCGA 10067
Qy 841 CCTCAGCTACAGCATCCTCGAAGGCTTCGGGAGACCCAGAAAGTTTCTCG--CCCTTAGA 899
Db 10068 CCTCAGCTACAGCATCCTCGAAGGCTTCGGGAGACCCAGAAAGTTTCTCGCCCTTAGA 10127
Qy 900 TCCAAACTTAGCAACCCGGAGTCTGGATTCTCTGGGAAGTCTCAGCTGTCTCGGGTTG 959
Db 10128 TCCAAACTTAGCAACCCGGAGTCTGGATTCTCTGGGAAGTCTCAGCTGTCTCGGGTTG 10187

Qy 960 TGCCGGGGCCCCCAGGCTCTGAGGGGACCACTGGCCGCTGTGGC 1001
Db 10188 TGCCGGGGCCCCCAGGCTCTGAGGGGACCACTGGCCGCTGTGGC 10229

RESULT 11
AAX88272
ID AAX88272 standard; DNA; 5126 BP.

XX AAX88272;
DT 22-SEP-1999 (first entry)
XX Human catalytic telomerase subunit 5'-flanking regulatory DNA.

XX Telomerase; subunit; human; regulatory; catalytic; anti-tumour; reporter;
KW modulator; telomerase regulatory region; cancer therapy; ss.
XX Homo sapiens.

XX DE19757984-A1.
XX 01-JUL-1999.
XX 24-DEC-1997; 97DE-01057984.

XX 24-DEC-1997; 97DE-01057984.
XX (FARB) BAYER AG.
XX Hagen G, Wick M, Zubov D;

XX WPI; 1999-372320/32.
XX New 5' flanking regulatory sequence from the human catalytic telomerase
PT subunit gene useful for cancer therapy.

XX Claim 1; Fig 4; 14pp; German.
XX This invention describes a novel 5' flanking regulatory sequence from the
CC human catalytic telomerase subunit gene. Recombinant constructs
CC containing the product of the invention can be linked with DNA encoding
CC an anti-tumour protein or reporter protein. The constructs are useful for
CC identifying candidate substances that modulate the activity of the
CC telomerase regulatory region. The constructs can be used in cancer
CC therapy

XX Sequence 5126 BP; 1009 A; 1532 C; 1404 G; 1180 T; 0 U; 1 Other;

Query Match 97.1%; Score 971.8; DB 2; Length 5126;
Best Local Similarity 99.4%; Pred. No. 2.4e-282;
Matches 996; Conservative 0; Mismatches 3; Indels 3; Gaps 2;

Qy 1 GGCTGGGATTACAGGACACCGCCACCATGCGCAGCTAATTTTGTATTTTGTAGTAGAGA 60
Db 3080 GGCTGGGATTACAGGACACCGCCACCATGCGCAGCTAATTTTGTATTTTGTAGTAGAGA 3139

Qy 61 CGGGGGTGGGGTGGGGTTTCCATGTTGGCCAGGCTGGTCTCGAATTTCTGACCTCAGA 120
Db 3140 CGGGGGT--GGGTGGGGTTTCCATGTTGGCCAGGCTGGTCTCGAATTTCTGACCTCAGA 3197

Qy 121 TGATCCACCTGCTCTGCCCTCTAAAGTGTGGGATTCAGGCTGTGAGCCACCATGCCCA 180
Db 3198 TGATCCACCTGCTCTGCCCTCTAAAGTGTGGGATTCAGGCTGTGAGCCACCATGCCCA 3257

Qy 181 GCTCAGAAATTACTCTGTTTAGAAACATCTGGGTCTCAGGTAGGAAGCTCACCCCACTCA 240
Db 3258 GCTCAGAAATTACTCTGTTTAGAAACATCTGGGTCTCAGGTAGGAAGCTCACCCCACTCA 3317

Qy 241 AGTGTCTGGGTGTTTAAAGCCAAATGATAGATTTTATTTTATTTTGTAGTACACTCTTGA 300
Db 3318 AGTGTCTGGGTGTTTAAAGCCAAATGATAGATTTTATTTTATTTTGTAGTACACTCTTGA 3377

QY 301 TGTTTTACATGTGATGACTAAGACATCATCAGCTTTTCAAAGACACACTAACTGCACCC 360
Db 3378 TGTTTTACATGTGATGACTAAGACATCATCAGCTTTTCAAAGACACACTAACTGCACCC 3437
QY 361 ATAACTACGGGGGTCTTCTCGGTATACAGCATCTTCATGTAATGCCGGGAGGCTTTCC 420
Db 3438 ATAACTACGGGGGTCTTCTCGGTATACAGCAATCTTCATGTAATGCCGGGAGGCTTTCC 3497
QY 421 TCGGCATGCACATGCTGTTAATTAATCTCCAGCATATCTTCGCTTCCATTTCTCTCTTC 480
Db 3498 TCGGCATGCACATGCTGTTAATTAATCTCCAGCATATCTTCGCTTCCATTTCTCTCTTC 3557
QY 481 CCTCTTTTAAATTTGTGTTTCTATGTTGGCTTCTCTGCAGAGAACCACTGTAAGCTACA 540
Db 3558 CCTCTTTTAAATTTGTGTTTCTATGTTGGCTTCTCTGCAGAGAACCACTGTAAGCTACA 3617
QY 541 ACTTAACCTTTTGTGGAAACAAATTTTCAAACCGCCCTTTGGCTTGTAGCGAGACAA 600
Db 3618 ACTTAACCTTTTGTGGAAACAAATTTTCAAACCGCCCTTTGGCTTGTAGCGAGACAA 3677
QY 601 TTCAACACACAGCCCTTTTAAAGGCTTAGGATCACTAAGGGGATTTCTAGAGAGCG 660
Db 3678 TTCAACACACAGCCCTTTTAAAGGCTTAGGATCACTAAGGGGATTTCTAGAGAGCG 3737
QY 661 ACCCGTAATCTTAAGTATTTTCAACAGACGAGCTTAACCTCCAGCGAGCGTGACAGCCACG 720
Db 3738 ACCGTGTAATCTTAAGTATTTTCAACAGACGAGCTTAACCTCCAGCGAGCGTGACAGCCACG 3797
QY 721 GAGGTGCGAGCCCTGTTCAAATGCTAGCTCCATAAATPAAAGCAATTTCTCCCGCAGTT 780
Db 3798 GAGGTGCGAGCCCTGTTCAAATGCTAGCTCCATAAATPAAAGCAATTTCTCCCGCAGTT 3857
QY 781 TCTGAAAGTAGAAGGTTTACATTTAAGTTGCGTTTGTGTTAGCATTTTCAGTTTGCCTGA 840
Db 3858 TCTGAAAGTAGAAGGTTTACATTTAAGTTGCGTTTGTGTTAGCATTTTCAGTTTGCCTGA 3917
QY 841 CCTCAGCTACAGCATCCCTGCAAGCCCTCGGAGACCCAGAGTTTCTTCG-CCCTTAGA 899
Db 3918 CCNAGCTACAGCATCCCTGCAAGCCCTCGGAGACCCAGAGTTTCTTCGCCCCCTTAGA 3977
QY 900 TCCAACTTGAGCAACCCGGAGTCTGATTTCTCGGAAAGTCTCAGCTGTCTCTCGGTTG 959
Db 3978 TCCAACTTGAGCAACCCGGAGTCTGATTTCTCGGAAAGTCTCAGCTGTCTCTCGGTTG 4037
QY 960 TGCCGGGGCCCGAGTCTGAGGGAGCCAGATGGCCGCTGTGGC 1001
Db 4038 TGCCGGGGCCCGAGTCTGAGGGAGCCAGATGGCCGCTGTGGC 4079

RESULT 12
ADV97952/c
ID ADV97952 standard; DNA; 2501 BP.
XX
AC ADV97952;
XX
DT 10-MAR-2005 (first entry)
XX
DE Human tumor-associated cancer-testis antigen tert DNA Seq 44.
XX
KW de; immunotherapy; DNA methylation; tumor-associated antigen; cancer;
KW cytostatic; vaccine; tert.
XX
OS Homo sapiens.
XX
PN EP1491639-A2.
XX
XX
PD 29-DEC-2004.
XX
XX 17-JUN-2004; 2004EP-00090238.
XX
PR 24-JUN-2003; 2003DE-01029240.

(EPIG-) EPIGENOMICS AG.

Eichler-Mertens M, Piepenbrock C, Olek A;

WPI; 2005-050366/06.

Identifying target points for immunotherapy of tumors by analysis of methylation status of many tumor-associated antigens, also treatment, particularly vaccination, using selected antigens.

Disclosure; SEQ ID NO 44; 206pp; German.

This invention relates to a novel method for determining target points for tumor immunotherapy by taking a DNA sample from serum or other bodily fluids of a patient. Specifically, it refers to identifying the methylation status of at least one CpG island in each of 47 identified tumor-associated antigens in order to generate a methylation pattern from the results. It describes an analysis of methylation status that includes chemical treatment of DNA with a bisulfite, optionally followed by amplification, particularly methylation specific PCR (MSP) and/ or a heavy methyl technique. Accordingly, the present invention provides tumor associated antigen sequences and also the corresponding bisulfite sequences generated under differing methylation conditions. As such, the method can be used to identify targets for immunotherapy of cancers, specifically by vaccination against selected tumor-associated antigens to provide individualized immunotherapy. Furthermore, the method allows simultaneous determination of methylation status of many tumor antigens and also of other methylation-regulated cofactors important for vaccination. The pharmaceutical compositions derived thereof exhibit cytostatic activity and can be used in the development of vaccines. This polynucleotide sequence is a human tumor associated cancer-testis antigen DNA sequence of the invention.

SEQ Sequence 2501 BP; 504 A; 767 C; 827 G; 403 T; 0 U; 0 Other;

Query Match 95.5%; Score 956; DB 14; Length 2501;

Best Local Similarity 100.0%; Pred. No. 1e-277;

Matches 956; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 46 TATTTTGTAGTAGACGGGGTGGGGTTCACCATGTTGGCCAGGCTGGTCTCGA 105

Db 2501 TATTTTGTAGTAGACGGGGTGGGGTTCACCATGTTGGCCAGGCTGGTCTCGA 2442

QY 106 ACTTCTGACCTCAGATGATCCACCTGCTCTGCTCTCTTAAAGTGTCTGAGATTACAGGTGT 165

Db 2441 ACTTCTGACCTCAGATGATCCACCTGCTCTGCTCTCTTAAAGTGTCTGAGATTACAGGTGT 2382

QY 166 GAGCCACCATGCCAGCTCAGAAATTTACTCTGTTTAGAAAACATCTGGGTCTGAGGTAGA 225

Db 2381 GAGCCACCATGCCAGCTCAGAAATTTACTCTGTTTAGAAAACATCTGGGTCTGAGGTAGA 2322

QY 226 AGCTCACCCCACTCAAGTGTGTGTGTTTAAAGCAATGATAGAAATTTTATTGTG 285

Db 2321 AGCTCACCCCACTCAAGTGTGTGTGTTTAAAGCAATGATAGAAATTTTATTGTG 2262

QY 286 TTAGAACACTCTGATGTTTACACTGTGATGACTAAGACATCATCAGCTTTTCAAAGAC 345

Db 2261 TTAGAACACTCTGATGTTTACACTGTGATGACTAAGACATCATCAGCTTTTCAAAGAC 2202

QY 346 ACACCTAACTGCACCCCAATAATCTGGGGTGTCTTCTGGGTATCAGCGATCTTCAATTGAATG 405

Db 2201 ACACCTAACTGCACCCCAATAATCTGGGGTGTCTTCTGGGTATCAGCGATCTTCAATTGAATG 2142

QY 406 CCGGAGGCGTTCCTCGCCATGCATGGGTGTGTTAAATTAATCTCCAGCATAAATCTTCGCTT 465

Db 2141 CCGGAGGCGTTCCTCGCCATGCATGGGTGTGTTAAATTAATCTCCAGCATAAATCTTCGCTT 2082

QY 466 CCATTTCTTCTCTCCCTCTTTTAAATTTGTTTCTATGTTGGTCTCTCTGCAGAGAA 525

Db 2081 CCATTTCTTCTCTCCCTCTTTTAAATTTGTTTCTATGTTGGTCTCTCTGCAGAGAA 2022

QY 526 CCAGTGTAAAGCTACAACTTAACCTTTGTTGGAAACAAATTTTCCAAACCGCCCTTTGCCC 585

QY 946 CTGTCCTCGCGTTGTGCGGGGCCCGCCAGAGTCTGAGGGGACCACTGGCCGCTGTGGC 1001
AAV16979
ID AAV16979 standard; DNA; 4335 BP.
XX
AC AAV16979;
XX
XX 13-AUG-1998 (first entry)
DT Human telomerase reverse transcriptase genomic clone.
XX
XX Human; telomerase reverse transcriptase; hTERT; TRT; diagnosis; prognosis;
KW cell proliferation; cancer; ageing; ribonucleoprotein; ss.
XX
XX Homo sapiens.
XX OS
XX GB2317891-A.
XX
XX 08-APR-1998.
XX
XX 01-OCT-1997; 97GB-00020890.
XX
XX 01-OCT-1996; 96US-00724643.
XX 18-APR-1997; 97US-00844419.
XX 25-APR-1997; 97US-00846017.
XX 06-MAY-1997; 97US-00851843.
XX 09-MAY-1997; 97US-00854050.
XX 14-AUG-1997; 97US-00911312.
XX 14-AUG-1997; 97US-00912951.
XX 14-AUG-1997; 97US-00915503.
XX
XX (GERO-) GERON CORP.
XX (UYTE-) UNIV TECHNOLOGY CORP.
XX
XX Cech TR, Lingner J, Nakamura T, Chapman KB, Morin GB, Harley CB;
XX Andrews WH;
XX WPI; 1998-171633/16.
XX
XX Pure and recombinant human Telomerase Reverse Transcriptase and its
XX variants - are useful in the diagnosis, prognosis and treatment of cell
XX proliferation conditions especially cancer and ageing.
XX
XX Example 3; Fig 21; 387pp; English.
XX
XX The present sequence represents a human telomerase reverse transcriptase
XX (hTERT) genomic clone from the present invention. The present invention
XX also describes the following methods: (A) determining whether a test
XX compound is a modulator of hTERT, by detecting the change in hTERT
XX recombinant protein or polynucleotide, on administration of the compound;
XX (B) preparation of recombinant telomerase by contacting a protein
XX preparation of hTERT with a telomerase RNA component; (C) detection of the
XX hTERT RNA or protein in a sample by binding a relevant probe to the sample
XX and detecting the complex formed or in the case of RNA detection,
XX amplifying the product and correlating the presence of complex or
XX amplification product with presence of hTERT in the sample; and (D)
XX increasing the proliferation of a vertebrate cell by increasing hTERT
XX expression; and (E) the use of an agent that causes an increase in cell
XX vertebrate cell proliferation to create a medicament that inhibits
XX ageing. A protein preparation of hTERT and the polynucleotide encoding
XX hTERT can be used in the manufacture of medicaments for inhibiting the
XX effect of ageing or cancer. Inhibitors of telomerase activity can be used
XX to treat conditions that are associated with high telomerase activity. A
XX protein preparation of hTERT can also be used in the new methods
XX
XX Sequence 4335 BP; 698 A; 1416 C; 1360 G; 861 T; 0 U; 0 Other;
SQ

Query Match 93.0%; Score 930.8; DB 2; Length 4335;
Best Local Similarity 99.1%; Pred. No. 5.5e-270;

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QY	1	GGCTGGGATTTACAGGACCCCGCCACCATGCCCAGCTAAATTTTGTATTTTGTAGTAGAGA	60							
Db	438	GGCTGGGATTTACAGGACCCCGCCACCATGCCCAGCTAAATTTTGTATTTTGTAGTAGAGA	497							
QY	61	CGGGGGTGGGGGTGGGGTTCAACATGTTGGCCAGGCTGGTCTCGAACTTCTGACCTCAGA	120							
Db	498	CGGGGGTGGGGGTGGGGTTCAACATGTTGGCCAGGCTGGTCTCGAACTTCTGACCTCAGA	557							
QY	121	TGATCCACCTGCTCTGCTCTTAAAGTGTGGGATTAACAGGTGTGAGGCCACCATGCCCA	180							
Db	558	TGATCCACCTGCTCTGCTCTTAAAGTGTGGGATTAACAGGTGTGAGGCCACCATGCCCA	617							
QY	181	GCTCAGAAATTTACTCTCTGTTTAGAAACATCTGGGTCTGAGGTAGGAAGCTCACCCCACTCA	240							
Db	618	GCTCAGAAATTTACTCTCTGTTTAGAAACATCTGGGTCTGAGGTAGGAAGCTCACCCCACTCA	677							
QY	241	AGTGTGTGTGTTTAAAGCCAAATGATAGAAATTTTATTTTATTTGTTGTAGAACACTCTTGA	300							
Db	678	AGTGTGTGTGTTTAAAGCCAAATGATAGAAATTTTATTTTATTTGTTGTAGAACACTCTTGA	737							
QY	301	TGTTTACACTGTGATGACTAAGACATCATCAGCTTTTCAAGACACACTAACTGCACCC	360							
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Db	798	ATAATACCTGGGTGCTCTTCTGGGTATCAGCGATCTTCAATGAAATCCGGGAGGGTTC	857							
QY	421	TGCGCATGCAATGGTGTAAATTAATCTCAGCATAACTTCTGCTTCCATTTCTCTCTTC	480							
Db	858	TGCGCATGCAATGGTGTAAATTAATCTCAGCATAACTTCTGCTTCCATTTCTCTCTTC	917							
QY	481	CTCTTTTAAATTTGTTTCTATGTTGGCTTCTCTGAGAGAACCAAGTGTAGCTACA	540							
Db	918	CTCTTTTAAATTTGTTTCTATGTTGGCTTCTCTGAGAGAACCAAGTGTAGCTACA	977							
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Db	978	ACTTAACTTTTGTGGAAACAAATTTTCCAAACCCCTTTCCTAGTGTGACAGACAA	1037							
QY	601	TTCAAAACACAGCCCTTTTAAAGGCTTAGGGATCACTAAGGGGATTTCTAGAGAGCG	660							
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Db	1338	CTTAGTCCAACTTGTAGCAACCCGGAGTCTGGATTCCTGGGAGTCTCTCAGCTGTCTCG	1397							
QY	954	CGGTGTGCGGGGCCCGCCAGGTCTGAGGGGACCAAGTGGCCGCTGTGGC 1001								
Db	1398	CGGTGTGCGGGGCCCGCCAGGTCTGAGGGGACCAAGTGGCCGCTGTGGC 1445								

RESULT 15
AAD27972/c

AD27972 standard; DNA; 35871 BP.
AD27972;
16-JUL-2002 (first entry)
Recombinant adenovirus vector KD3-TERT.
Recombinant adenovirus vector; adenovirus death protein; ADP; telomerase;
human; telomerase reverse transcriptase promoter; TERT; neoplastic cell;
cancer; KD3-TERT; E1A region; mutant; ds.
Mastadenovirus.
Homo sapiens.
Synthetic.
Chimeric.
US2002028785-A1.
07-MAR-2002.
19-SEP-2001; 2001US-00956335.
12-JUL-1999; 99US-00351778.
20-SEP-2000; 2000US-0233872P.
(UYSL-) UNIV SAINT LOUIS.
Wold WSM, Toth K, Tollefson AE, Kuppuswamy M;
WPI; 2002-328910/36.
Novel recombinant adenovirus vector useful for destroying neoplastic
cells, comprises a human telomerase reverse transcriptase promoter and at
least one inactivation mutation in the E3 region.
Claim 5; Page 28-44; 64pp; English.
The invention relates to a recombinant adenovirus vector which
overexpresses an adenovirus death protein (ADP) and which is replication-
restricted to cells expressing telomerase, comprises a human telomerase
reverse transcriptase promoter (hTERT) and at least one inactivating
mutation in the E3 region. The vector of the invention is useful in vitro
for promoting death of a cell expressing telomerase, and for promoting
death of neoplastic cells in a patient. The adenovirus vector is an
efficient and effective anticancer agent that could specifically target
neoplastic cells, while replicating poorly or not at all in normal
tissue, and efficiently spreading to neighbouring neoplastic cells,
thereby maximising its cancer-killing ability. The presence of human
telomerase reverse transcriptase promoter allows restriction of
replication of the adenovirus to cells expressing telomerase without the
need for complementation to achieve replication competence in these
cells. The present sequence is adenovirus vector KD3-TERT which comprises
an ADP gene, a hTERT promoter, and a mutation in the E1A region
Sequence 35871 BP; 8238 A; 10114 C; 10001 G; 7518 T; 0 U; 0 Other;
Query Match 67.7%; Score 677.8; DB 6; Length 35871;
Best Local Similarity 99.7%; Pred. No. 4.7e-193;
Matches 679; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 321 AAGCATCATCAGCTTTTCAAGACACACTAACTGACCCCATATACTATCTGCTCTCT 380
Db 35713 AAGTAATCATCAGCTTTTCAAGACACACTAACTGACCCCATATACTATCTGCTCTCT 35654
Qy 381 GGGTATCAGCATCTTCATTAAGCCGGAGGGGTTTCTCGCCATGCATGGTGTTA 440
Db 35653 GGGTATCAGCATCTTCATTAAGCCGGAGGGGTTTCTCGCCATGCATGGTGTTA 35594
Qy 441 ATTACTCCAGCATATCTTCGTCTCCATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 500
Db 35593 ATTACTCCAGCATATCTTCGTCTCCATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 35534

Qy 501 TCTATGTTGGCTTCTCTGACAGAGCAACAGTGTAAGCTTACACTTTTGTGGGAACA 560
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Qy 561 AATTTTCCAAACCGCCCTTTGCCCCTAGTGCGCAGAGACAATTCACAAACACAGCCCTTTTA 620
Db 35473 AATTTTCCAAACCGCCCTTTGCCCCTAGTGCGCAGAGACAATTCACAAACACAGCCCTTTTA 35414
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Db 35413 AAAAGGCTTAGGATCACTAAGGGGATTTCTAGAGAGCGACCCGTTAATCTTAAGTATTT 35354
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Qy 801 CATTTAAGGTTGCGTTTGTAGCATTTTCAGTGTTCGCGACCTCAGCTACAGCATCCCTG 860
Db 35233 CATTTAAGGTTGCGTTTGTAGCATTTTCAGTGTTCGCGACCTCAGCTACAGCATCCCTG 35174
Qy 861 CAAGGCTCGGAGAGCCAGAGTTTCTCGCCCTTAGATCCAAACTTGAGCAACCCGGA 920
Db 35173 CAAGGCTCGGAGAGCCAGAGTTTCTCGCCCTTAGATCCAAACTTGAGCAACCCGGA 35114
Qy 921 GTCTGATTCTCGGAAAGTCTCAGCTGTCTCGGGTTGTGCGGGGCCCCCAGGCTCTGGA 980
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Qy 981 GGGGACCAAGTGGCGGTGGC 1001
Db 35053 GGGGACCAAGTGGCGGTGGC 35033

Search completed: January 10, 2006, 11:12:06
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OM nucleic - nucleic search, using sw model

Run on: January 10, 2006, 10:08:59 ; Search time 5387 Seconds
(without alignments)

10562.520 Million cell updates/sec

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Scoring table: IDENTITY NUC

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Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_in.*

3: gb_env.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pr.*

9: gb_ro.*

10: gb_sts.*

11: gb_sy.*

12: gb_un.*

13: gb_vl.*

14: gb_htg.*

15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1001	100.0	4321	6 AR390473	AR390473 Sequence
2	1001	100.0	15332	8 AF121948	AF121948 Homo sapi
3	1001	100.0	15418	6 AR342806	AR342806 Sequence
4	1001	100.0	15418	6 AR490112	AR490112 Sequence
5	1001	100.0	15418	6 AR576878	AR576878 Sequence
6	1001	100.0	15418	6 AX453025	AX453025 Sequence
7	1001	100.0	15418	6 AX498409	AX498409 Sequence
8	1001	100.0	15418	6 AX504952	AX504952 Sequence
9	1001	100.0	92564	8 AY007685	AY007685 Homo sapi
10	1001	100.0	161252	14 AC114955	AC114955 Homo sapi
11	999.4	99.8	202305	8 AC114931	AC114931 Homo sapi
12	989.8	98.9	170646	14 AC123545	AC123545 Pan trogl
13	989	98.8	4356	8 AF097365	AF097365 Homo sapi
14	972.8	97.2	5126	6 AX003120	AX003120 Sequence
15	972.8	97.2	5491	8 AB016767	AB016767 Homo sapi
16	972.8	97.2	11276	6 AX003122	AX003122 Sequence
17	972.8	97.2	26414	8 HSTER11	AF128893 Homo sapi
18	972.8	97.2	51552	6 AR266023	AR266023 Sequence

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c	21	930.8	93.0	4335	6	E36796	Human telom
c	22	930.8	93.0	4335	6	AR393087	Sequence
c	23	930.8	93.0	4335	6	AX810041	Sequence
c	24	930.8	93.0	4335	6	BD011047	Human tel
c	25	916.6	91.6	12213	8	AF114847	AF114847 Homo sapi
c	26	815.4	81.5	170946	14	AC117933	AC117933 Papio anu
c	27	815.4	81.5	183506	14	AC122155	AC122155 Papio anu
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ALIGNMENTS

RESULT 1	AR390473	AR390473	4321 bp	DNA	linear	PAT 18-DEC-2003
LOCUS	Sequence 6 from patent US 6610839.					
DEFINITION	AR390473					
ACCESSION	AR390473.1	GI:40112397				
VERSION						
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1 (bases 1 to 4321)					
AUTHORS	Morin, G.B. and Andrews, W.H.					
TITLE	Promoter for telomerase reverse transcriptase					
JOURNAL	Patent: US 6610839-A 6 26-AUG-2003;					
FEATURES	Location/Qualifiers					
source	1..4321					
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	/mol_type="genomic DNA"					

Query Match	100.0%	Score	1001;	DB	6;	Length	4321;
Best Local Similarity	100.0%	Pred. No.	4.8e-280;				
Matches	1001;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
Qy	1	GGCTGGGATTACAGCACC	CGCCCGCCAGCTAAATTTTCTATTTTAGTAGAGA	60			
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Qy	61	CGGGGGTGGGGTGGGGT	TCACCATGTTGGCCAGGCTGCTCGAACTTCTGACCTCAGA	120			
Db	498	CGGGGGTGGGGTGGGGT	TCACCATGTTGGCCAGGCTGCTCGAACTTCTGACCTCAGA	557			
Qy	121	TGATCCACCTGCCTCTGCT	CTCTAAAGTGTGGGATTCAGGTGTGAGCCACCATGCCCA	180			
Db	558	TGATCCACCTGCCTCTGCT	CTCTAAAGTGTGGGATTCAGGTGTGAGCCACCATGCCCA	617			
Qy	181	GCTCAGATTACTCTGTTT	AGAAACATCTGGGCTCTGAGGTAGGAAGCTCACCCCACTCA	240			
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Qy |||||
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RESULT 2
AF121948 15332 bp DNA linear PRI 11-APR-1999
LOCUS Homo sapiens telomerase reverse transcriptase (TERT) gene, partial cds.
DEFINITION
ACCESSION AF121948
VERSION AF121948.1 GI:4580662
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 15332)
AUTHORS Greenberg, R.A., O'Hagan, R.C., Deng, H., Xiao, Q., Hann, S.R., Adams, R.R., Lichtsteiner, S., Chin, L., Morin, G.B. and DePinho, R.A.
TITLE Telomerase reverse transcriptase gene is a direct target of c-Myc but is not functionally equivalent in cellular transformation
JOURNAL Oncogene 18 (5), 1219-1226 (1999)
PUBMED 10022128

REFERENCE 2 (bases 1 to 15332)
AUTHORS Morin, G.B., Carlos, R. and Adams, R.R.
TITLE Direct Submission
JOURNAL Submitted (21-JAN-1999) Geron Corporation, 230 Constitution Drive, Menlo Park, CA 94025, USA
FEATURES
Location/Qualifiers
source 1..15332
/organism="Homo sapiens"
/mol_type="genomic DNA"
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gene 1..>15332
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promoter 1..13446
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CDS join(13502..13720,13825..>15178)
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ORIGIN
Query Match 100.0%; Score 1001; DB 8; Length 15332;
Best Local Similarity 100.0%; Pred. No. 5.5e-280;
Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 11517 CGGGGTGGGGGTGGGGTTCACCATGTCGCCAGGCTGCTCGAACTCTGACCTCAGA 11576
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Db 11577 TGATCCACCTGCTCTGCTCTCTAAAGTGTCTGGGATTTACAGGTGTGAGCCACCATGCCA 11636
Qy 181 GCTCAGAAATTTACTCTGTTTAGAAACATCTGGGTCTGAGGTAGGAGCTCACCCACTCA 240
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Qy 241 AGTGTCTGCTGTTTAAAGCAATGATAGAAATTTTATTTATTTGTTAGAACACTCTTGA 300
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Db 11757 TGTGTTTACACTGTGATGATCACTAAGACATCATCAGCTTTTCAAGACACACTAACTGCACCC 11816
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Db |||||

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RESULT 3
AR342806
LOCUS AR342806 15418 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 1 from patent US 6576464.
ACCESSION AR342806
VERSION AR342806.1 GI:33738009
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15418)
AUTHORS Gold, J.D. and Lebkowski, J.S.
TITLE Methode for providing differentiated stem cells
JOURNAL Patent: US 6576464-A 1 10-JUN-2003;
Geron Corporation; Menlo Park, CA
FEATURES
Location/Qualifiers
source 1..15418
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ORIGIN
Query Match 100.0%; Score 1001; DB 6; Length 15418;
Best Local Similarity 100.0%; Pred. No. 5.5e-280;
Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 61 CGGGGGTGGGGTGGGGTTCACATGTTGGCCAGGCTGCTCGAACTTCTGACCTCAGA 120
Db 11560 CGGGGGTGGGGTGGGGTTCACATGTTGGCCAGGCTGCTCGAACTTCTGACCTCAGA 11619
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Db 11620 TGATCCACCTGCCTCTGCCTCTCTAAAGTGTGGGATTACAGGTGTGAGCCACCATGCCCA 11679
Qy 181 GCTCAGAAATTTACTCTGTTTAAAGATCTGGGTCTGAGGTAGGAAGCTACCCCACTCA 240
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Qy 301 TGTTTTACACTGTGATGACTAAGACATCATCAGCTTTTCAAAGACACACTAACTGCACCC 360
Db 11800 TGTTTTACACTGTGATGACTAAGACATCATCAGCTTTTCAAAGACACACTAACTGCACCC 11859
Qy 361 ATAATACCTGGGTGTCTTCTGGGTATCAGGATCTTCAATGAATCCGGGAGGCGTTTCC 420
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Db 12160 ACCGGTAATCTTAAGTATTTTACAGAGAGAGGCTAACTCCAGCGAGCTGACAGCCAGG 12219
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RESULT 4
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LOCUS AR490112 15418 bp DNA linear PAT 15-MAY-2004
DEFINITION Sequence 1 from patent US 6713055.
ACCESSION AR490112
VERSION AR490112.1 GI:47257268
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15418)
AUTHORS Schiff, J.M.
TITLE Glycosyltransferase vectors for treating cancer
JOURNAL Patent: US 6713055-A 1 30-MAR-2004;
Geron Corporation; Menlo Park, CA
FEATURES
Location/Qualifiers
source 1..15418
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ORIGIN

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Query Match      100.0%; Score 1001; DB 6; Length 15418;
Best Local Similarity 100.0%; Pred. No. 5.5e-280;
Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 241 AGTGTGTGTGTGTTTAAAGCAATGATAGAAATTTTATTTTGTAGAACACTCTTTGA 300
Db 11740 AGTGTGTGTGTGTTTAAAGCAATGATAGAAATTTTATTTTGTAGAACACTCTTTGA 11799

Qy 301 TGTTTTACACTGTGATGACTTAAGCAATCATCAGCTTTTCAAAGACACACTAACTGCACCC 360
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Qy 361 ATAATACCTGGGGTCTCTTGGGTATCAGGATCTTCAATGAATCGCGGAGGGTTTCC 420
Db 11860 ATAATACCTGGGGTCTCTTGGGTATCAGGATCTTCAATGAATCGCGGAGGGTTTCC 11919

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RESULT 5
LOCUS AR576878 15418 bp DNA linear PAT 14-DEC-2004
DEFINITION Sequence 1 from patent US 6777203.
ACCESSION AR576878
VERSION AR576878.1 GI:56579198
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 15418)
AUTHORS Morin,G.B.; Lichtsteiner,S.P.; Vasserot,A.P.; Adams,R.R. and
Andrews,W.H.
TITLE Telomerase promoter driving expression of therapeutic gene
sequences
JOURNAL Patent: US 6777203-A 1 17-AUG-2004;
Geron Corporation; Menlo Park, CA
FEATURES
source
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ORIGIN

Query Match      100.0%; Score 1001; DB 6; Length 15418;
Best Local Similarity 100.0%; Pred. No. 5.5e-280;
Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGCTGGGATTACAGGACCGCCACCATGCGCCAGCTAAATTTTGTATTTTAGTAGAGA 60
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Qy 781 TCTGAAGATAGGAAGGTTACATTTAAGGTTGCGTTTGTAGCAATTTTCAAGTGTGCGGA 840
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LOCUS AX453025 15418 bp DNA linear PAT 06-JUL-2002
DEFINITION Sequence 1 from Patent WO0242445.
ACCESSION AX453025
VERSION AX453025.1 GI:21712594
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Gold, J.D. and Lebkowski, J.S.
TITLE Differentiated cells suitable for human therapy
JOURNAL Patent: WO 0242445-A 1 30-MAY-2002;
Geron Corporation (US)
FEATURES
source Location/Qualifiers
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ORIGIN

Query Match 100.0%; Score 1001; DB 6; Length 15418;
Best Local Similarity 100.0%; Pred. No. 5.5e-280;
Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 7
LOCUS AX498409 15418 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 1 from Patent WO02053760.
ACCESSION AX498409
VERSION AX498409.1 GI:23343287
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Irving, J.M. and Lebkowski, J.S.
TITLE Chimeric cytolytic viruses for cancer treatment
JOURNAL Patent: WO 02053760-A 1 11-JUL-2002;
Geron Corporation (US)
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QY	61	CGGGGGTGGGGGTGGGGGTTCACCATGTGCGCCAGGCTGCTTCGAACCTTCTCACTCTCAGCTCAGA	120	
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QY	121	TGATCCACCTGCCTCTGCCTCTCTAAAGTCTCGGATTCAGAGTGTGAGCCACCATGCCCA	180	
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QY	181	GCTCAGAAATTTACTCTGTTTAGNAAACATCTGGGTCTGAGGTAGGAAGCTCACCCCACTCA	240	
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QY	361	ATAATCTGGGGTGTCTTCTGGGTATCAGCGATCTTCATGTGAATGCGGGAGGCGTTCC	420	
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QY	781	TCGTAAAGTAGGAAAGGTTACATTTAAGTGTGGTTTGTATGATTTTCAGTGTTCGCCGA	840	
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Qy 781 TCTGAAGTAGGAAGGTTACATTTAGGTTGCGTTTGTAGCATTTTCAGTGTTCGCGA 840
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RESULT 9
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LOCUS Homo sapiens telomerase catalytic subunit (TERT) and sodium
DEFINITION channel-like protein genes, complete cds.
ACCESSION AY007685
VERSION AY007685.2 GI:15991796
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo
REFERENCE 1 (bases 1 to 92564)
Leem,S.H., Londono-Vallejo,J.A., Kim,J.H., Bui,H., Tubacher,E.,
Solomon,G., Park,J.E., Horikawa,I., Kouprina,N., Barrett,J.C. and
Larionov,V.
The human telomerase gene: complete genomic sequence and analysis
of tandem repeat polymorphisms in intronic regions
JOURNAL Oncogene 21 (5), 769-777 (2002)
PUBMED 11850805
REFERENCE 2 (bases 1 to 92564)
Londono-Vallejo,J.A.
JOURNAL Direct Submission
TITLES Submitted (06-SEP-2000) Centre d'Etudes du Polymorphisme Humain, 27
rue Juliette Dodu, Paris 75010, France
3 (bases 1 to 92564)
Londono-Vallejo,J.A.
JOURNAL Direct Submission
TITLES Submitted (10-OCT-2001) Centre d'Etudes du Polymorphisme Humain, 27
rue Juliette Dodu, Paris 75010, France
REMARK Sequence update by submitter
COMMENT On Oct 10, 2001 this sequence version replaced gi:12642956.
FEATURES
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Db 137865 GAGGGTCGAGGCGCTGTTCAATGCTAGCTCCATAATAAGCAATTTCTCCGGCAGTT 137806

Qy 781 TCTGAAAGTAGGAAAGGTTACATTTAAGGTTCGCTTTGTTAGCATTTTCAGTGTTCGCCGA 840

Db 137805 TCTGAAAGTAGGAAAGGTTACATTTAAGGTTCGCTTTGTTAGCATTTTCAGTGTTCGCCGA 137746

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Qy 901 CCAAACTTGAGCAACCCGGAGTCTGGATTCTCTGGGAAGTCTCAGCTGTCTCGGTTGT 960

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Qy 961 GCCGGGCCCCAGCTCTGGAGGGACACAGTGGCGTGTGGC 1001

Db 137625 GCCGGGCCCCAGCTCTGGAGGGACACAGTGGCGTGTGGC 137585

RESULT 11

AC114291/c 202305 bp DNA linear PRI 15-MAR-2003

LOCUS AC114291

DEFINITION Homo sapiens chromosome 5 clone CTD-3080P12, complete sequence.

ACCESSION AC114291

VERSION AC114291.2 GI:28973811

KEYWORDS HTG.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 202305)

DOE Joint Genome Institute and Stanford Human Genome Center.

Direct Submission

Unpublished

2 (bases 1 to 202305)

DOE Joint Genome Institute.

Direct Submission

Submitted (07-MAR-2002) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

3 (bases 1 to 202305)

DOE Joint Genome Institute and Stanford Human Genome Center.

Direct Submission

Submitted (15-MAR-2003) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

On Mar 15, 2003 this sequence version replaced gi:19224940..

Draft Sequence Produced by DOE Joint Genome Institute

www.jgi.doe.gov

Finishing Completed at Stanford Human Genome Center

www-shgc.stanford.edu

Quality: Phrap Quality >=40 99.9% of Sequence;

Estimated Total Number of Errors is 0.2.

NOTE: Transposon sequencing failed to verify number of repeat copies 173000-175780. Unsure number of repeat copies 173000-175780. BAC and subclones unstable 76080. Force join at 76080.

Location/Qualifiers

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Qy 61 CGGGGGTGGGGGTGGGGTTACCATGTTGGCCAGGCTGGTCTCGAACTTCTGACCTCAGA 120

Db 180981 CGGGGGTGGGGGTGGGGTTACCATGTTGGCCAGGCTGGTCTCGAACTTCTGACCTCAGA 180922

Qy 121 TGATCCACCTGCGCTCTGCCCTCCTAAAGTCTCGGATTTACAGGTGTGAGCCACCATGCCCA 180

Db 180921 TGATCCACCTGCGCTCTGCCCTCCTAAAGTCTCGGATTTACAGGTGTGAGCCACCATGCCCA 180862

Qy 181 GCTCAGAAATTTACTCTCTGTTTAAAGAACATCTGGGTCTGAGGTAGGAAGCTCACCCCACTCA 240

Db 180861 GCTCAGAAATTTACTCTCTGTTTAAAGAACATCTGGGTCTGAGGTAGGAAGCTCACCCCACTCA 180802

Qy 241 AGTGTGTGGTGTGTTTAAAGCAATGATAGAAATTTTATTTTATTTTGTAGAACTCTTTGA 300

Db 180801 AGTGTGTGGTGTGTTTAAAGCAATGATAGAAATTTTATTTTATTTTGTAGAACTCTTTGA 180742

Qy 301 TGTTTTTACACTGTGATGACTTAAGACATCATCAGCTTTTCAAAGACACACTAACTGACACC 360

Db 180741 TGTTTTTACACTGTGATGACTTAAGACATCATCAGCTTTTCAAAGACACACTAACTGACACC 180682

Qy 361 ATAATACTGGGGTGTCTCTGGGTATCAGCGATCTTCATTGAATTCGCCGGAGGGGTTTCC 420

Db 180681 ATAATACTGGGGTGTCTCTGGGTATCAGCGATCTTCATTGAATTCGCCGGAGGGGTTTCC 180622

Qy 421 TCGCCATGCAATGCTGTTTAAATTTACTCCAGCATAAATCTCTGCTTCCATTTCTTCTTTC 480

Db 180621 TCGCCATGCAATGCTGTTTAAATTTACTCCAGCATAAATCTCTGCTTCCATTTCTTCTTTC 180562

Qy 481 CTTCTTTTAAATTTGTTTCTCTATGTTGGTCTCTGCGAGAGAACAGGTGAAGCTACA 540

Db 180561 CTTCTTTTAAATTTGTTTCTCTATGTTGGTCTCTGCGAGAGAACAGGTGAAGCTACA 180502

Qy 541 ACTTAACCTTTTGTGGAAACAAATTTTCCAAACCGCCCTTTTGCCTAGTGGCAGAGACAA 600

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Qy 601 TTCACAAACACAGCCCTTTTAAAGGCTTAGGGATCATAAGGGGATTTCTAGAGAGCG 660

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Db 180381 ACCGTAATCCTAAGTATTACAGACAGGCTTAACCTCAGCGAGGCTGACAGCCAGG 180322

Qy 721 GAGGGTCGAGGCGCTGTTCAATGCTAGCTCCATAATAAGCAATTTCTCCGGCAGTT 780

Db 180321 GAGGGTCGAGGCGCTGTTCAATGCTAGCTCCATAATAAGCAATTTCTCCGGCAGTT 180262

Qy 781 TCTGAAAGTAGGAAAGGTTACATTTAAGGTTCGCTTTGTTAGCATTTTCAGTGTTCGCCGA 840

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RESULT 12
 AC123545/c
 LOCUS
 DEFINITION Pan troglodytes clone RP43-165N9, WORKING DRAFT SEQUENCE, 10
 ordered pieces.
 AC123545
 AC123545.3 GI:33235839
 HTG; HTGS PHASE2; HTGS DRAFT.
 SOURCE Pan troglodytes (chimpanzee)
 ORGANISM Pan troglodytes
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Pan.
 REFERENCE
 1 (bases 1 to 170646)
 Antonellis, A., Ayele, K., Becketrom-Sternberg, S.M., Benjamin, B.,
 Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooke, S., Cariaga, K.,
 Chu, G., Coleman, B., Coleman, H., Engle, J., Granite, S., Guan, X.,
 Gupta, J., Haghighi, P., Han, J., Hansen, N., Ho, S.-L., Hu, P.,
 Hurlle, B., Idol, J.R., Karlins, E., Kwong, P., Laric, P., Lee-Lin, S.-Q.,
 Legaspi, R., Maduro, Q.L., Maduro, V.B., Margulies, E.H., Masiello, C.,
 Maskai, B., McDowell, J., Paguirigan, C., Pearson, R., Portnoy, M.R.,
 Prasad, A., Reddix-bugue, N., Schandler, K., Schueler, M.G., Shah, K.,
 Vost, C., Stantripp, S., Thomas, J.W., Thomas, P.J., Tsipouri, V.,
 Vogt, J.L., Wetherby, K.D., Young, A. and Green, E.D.
 NISC Comparative Sequencing Initiative
 Unpublished
 2 (bases 1 to 170646)
 Green, E.D.
 Direct Submission
 Submitted (30-MAY-2002) NIH Intramural Sequencing Center, 8717
 Government Circle, Gaithersburg, MD 20877, USA
 3 (bases 1 to 170646)
 Green, E.D.
 Direct Submission
 Submitted (25-JUL-2003) NIH Intramural Sequencing Center, 8717
 Government Circle, Gaithersburg, MD 20877, USA
 On Jul 25, 2003 this sequence version replaced gi:24414279.
 ----- Genome Center
 Center: NIH Intramural Sequencing Center
 Center code: NISC
 Web site: <http://www.nisc.nih.gov>
 Contact: nisc.zoo@nhgri.nih.gov
 ----- Project Information
 Center project name: cmz
 Center clone name: 165N09

The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8X average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.
 ----- Summary Statistics
 Sequencing vector: plasmid; n/a; 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.990319
 Consensus quality: 16710 bases at least Q40
 Consensus quality: 168559 bases at least Q30
 Consensus quality: 169363 bases at least Q20
 Insert size: 152000; agarose-fp
 Insert size: 169746; sum-of-contigs

Quality coverage: 11.31x in Q20 bases; agarose-fp
 Quality coverage: 10.13x in Q20 bases; sum-of-contigs

 * NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have been provided by the submitter.
 * This sequence will be replaced
 * by the finished sequence as soon as it is available and
 * the accession number will be preserved.
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 * 6385: gap of unknown length
 * 37411: contig of 30927 bp in length
 * 37412: gap of unknown length
 * 37512: contig of 8840 bp in length
 * 46451: gap of unknown length
 * 46452: contig of 5365 bp in length
 * 51817: gap of unknown length
 * 51917: contig of 16060 bp in length
 * 67977: gap of unknown length
 * 68077: contig of 46604 bp in length
 * 114681: gap of unknown length
 * 114682: contig of 6871 bp in length
 * 121652: gap of unknown length
 * 121751: contig of 4180 bp in length
 * 125932: gap of unknown length
 * 126032: contig of 2325 bp in length
 * 128357: gap of unknown length
 * 128457: contig of 42190 bp in length.
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Qy 92137 GGCTGGGATTACAGGACCCGCGCACCATGCGCAGCTAAATTTTGTATTTTGTAGTAGAGA 92078
Db |
Qy 61 CGGGGGTGGGGTGGGGTTCACCATGTTGGCCAGGCTGCTCGAACTTCTGACCTCAGA 120
Db CGGGGGTGGGGTGGGGTTCACCATGTTGGCCAGGCTGCTCGAACTTCTGACCTCAGA 92018
Qy 121 TGATCCACCTGCCTCTGCCCTCTAAAGTGTGGGATTACAGGTGTGAGCCACCATGCCCA 180
Db TGATCCACCTGCCTCTGCCCTCTAAAGTGTGGGATTACAGGTGTGAGCCACCATGCCCA 91958
Qy 181 GCTCAGAAATTTACTCTCTTTAGAAACATCTGGGTCTGAGGTAGGAGCTCACCCACTCA 240
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Qy 421 TCGCCATGCAATGGTGTAAATTAATTCACGACATAATCTCTGCTTCCATTTCTCTCTTC 480
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Db CCTCTTTTAAATTTGTTTCTATGTTGCTTCTGCGAGAGAACAGTGAAGTACA 91598
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RESULT 13
AF097365
LOCUS
DEFINITION Homo sapiens telomerase reverse transcriptase (TERT) gene, promoter
and partial cds.
ACCESSION AF097365
VERSION AF097365.1 GI:4210970
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
MAMMALIA; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 4356)
AUTHORS Cong, Y.S., Wen, J. and Bacchetti, S.
TITLE The human telomerase catalytic subunit hTERT: organization of the
gene and characterization of the promoter
JOURNAL Hum. Mol. Genet. 8 (1), 137-142 (1999)
PUBMED 9887342
REFERENCE 2 (bases 1 to 4356)
AUTHORS Cong, Y.S., Wen, J. and Bacchetti, S.
TITLE Direct Submission
JOURNAL Submitted (05-OCT-1998) Pathology, McMaster University, 1200 Main
St. W., Hamilton, ON L8N 3Z5, Canada
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DEFINITION Sequence 1 from Patent WO9933998.
ACCESSION AX003120
VERSION AX003120.1 GI:9926982
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
Wick, M. and Hagen, G.
AUTHORS
TITLE Regulatory dna sequences of the human catalytic telomerase sub-unit
gene, diagnostic and therapeutic use thereof
JOURNAL Patent: WO 9933998-A 1 08-JUL-1999;
WICK MARESA (DE); BAYER AG (DE)

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Best Local Similarity 99.5%; Pred. No. 8e-272;
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RESULT 15

AB016767

LOCUS AB016767 5491 bp DNA linear PRI 29-JAN-2002

DEFINITION Homo sapiens gene for telomerase transcriptase, partial cdb.

ACCESSION AB016767

VERSION AB016767.1 GI:4239869

KEYWORDS telomerase transcriptase; hTERT.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

1

REFERENCE

AUTHORS Takakura,M., Kyo,S., Kanaya,T., Hirano,H., Takeda,J., Yutsudo,M. and Inoue,M.

TITLE Cloning of human telomerase catalytic subunit (hTERT) gene promoter and identification of proximal core promoter sequences essential for transcriptional activation in immortalized and cancer cells

JOURNAL Cancer Res. 59 (3), 551-557 (1999)

PUBMED 9973199

REFERENCE

AUTHORS Takakura,M., Kyo,S., Kanaya,T., Takeda,J. and Inoue,M.

TITLE Direct Submission

JOURNAL Submitted (04-AUG-1998) Masahiro Takakura, Kanazawa University, School of Medicine, Department of Obstetrics and Gynecology; 13-1, Takaramachi, Kanazawa, Ishikawa 920-0934, Japan

(E-mail:takakura@med.kanazawa-u.ac.jp, Tel:81-76-265-2425, Fax:81-76-234-4266)

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Query Match 97.2%; Score 972.8; DB 8; Length 5491;

Best Local Similarity 99.5%; Pred. No. 8.1e-272;

Matches 997; Conservative 0; Mismatches 2; Indels 3; Gaps 2;

Qy 1 GGCTGGGATTACAGGCACCGCCACCATGCCCAGCTAAATTTTGTATTTTGTATTTAGTATGAGA 60

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Db 1609 AGTGTGTGGTGTGTTTAAAGCCATGATAGAAATTTTATTTTATTTGTTGTAGAACACTCTTGA 1668

Qy 301 TGTTTTTACACTGTGATGACTAAGACATCATCAGCTTTTCAAAGACACACTAACTGCACCC 360

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Qy 541 ACTTAACTTTTGTGGAAACAAATTTTCCAAACCGCCCTTTGCTAGTGGGAGAGACAA 600

Db 1909 ACTTAACTTTTGTGGAAACAAATTTTCCAAACCGCCCTTTGCTAGTGGGAGAGACAA 1968

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 10, 2006, 05:49:50 ; Search time 4711 Seconds
(without alignments)
9941.386 Million cell updates/sec

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Gapop 10.0 , Gapext 1.0

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	56.2	5.6	410	2 BF873304	BF873304 CM0-ET012
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C 4	52	5.2	541	6 CP790496	CP790496 875629 MA
C 5	50.8	5.1	660	10 C8820739	C8820739 tigr-gss-
C 6	50.2	5.0	976	5 BQ707318	BQ707318 AGENCOURT
C 7	50	5.0	825	6 CD653180	CD653180 AGENCOURT
C 8	49.2	4.9	525	9 AQ405885	AQ405885 HS_5043 B
C 9	48.4	4.8	439	9 AQ112190	AQ112190 CIT-HSP-2
C 10	47.8	4.8	313	2 BG952375	BG952375 PM4-CT056
C 11	47.6	4.8	780	9 CC539630	CC539630 CH240_419
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C 15	45.6	4.6	791	10 CL003114	CL003114 gbel VM5
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C 17	45.4	4.5	625	7 CO616290	CO616290 DG9-155J5
C 18	45.4	4.5	868	5 BX422116	BX422116 BX422116
C 19	44.8	4.5	651	10 CL323295	CL323295 RPCI44_45
C 20	44.8	4.5	1116	5 BX404837	BX404837 BX404837
C 21	44.8	4.5	1120	5 BX404704	BX404704 BX404704
C 22	44.6	4.5	688	5 BX674306	BX674306 BX674306

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ALIGNMENTS

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LOCUS Pan troglodytes DNA, clone: PTB-002L10.R, genomic survey sequence.
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VERSION AG030352.1 GI:16557225
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SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominae; Pan.
REFERENCE 1
AUTHORS Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE BAC end sequences of Library PTB
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 752)
AUTHORS Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE Direct Submission
JOURNAL Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-cho,Tsukumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:chimbese@sc.riken.go.jp, URL:http://hgp.sec.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the Rad process and may have higher chance of
clone tracking errors.
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LIBRARY
Vector : pKS145
R.Site 1 : SacI
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FEATURES

source

ORIGIN

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Db	303	TGGATCATCTGAGAGGCCCTTTTATAAATACAGAGTCCTTATAAAAGGGAGACAGAAAGG	362
QY	698	GTCAAGAGGGGGGAGCCCTCAGGACGATGAGGAGCAGTCAGTCTCAGGCTGAAAAGGGAGGG	757
Db	363	CTCAGATCAGGGGAGATTGAGATGCTGCCCTGTTGGTTTTGGAGTTGAGAGAGA-	421
QY	758	AGGCGCTTCGAGCCAGCGCTTCGAAGCCCTCCAGAGCTCGAAAGAAAGCGGGGAAGGGACC	817
Db	422	--GCGCTTGGGCCCAAGAAATTCGAGCGAGCTTCTTGAGCTGGAAGACCCAGAAACACATT	479
QY	818	CTCCAC--GGAGCCTGCAGCAGGAGGACACGGCTG	850
Db	480	TTCTCTTAGAGCCTCCAGGAGGAGCACAGCTCTG	513
RESULT 6			
BQ707318/c			
LOCUS	BQ707318	976 bp	mRNA
DEFINITION	AGENCOURT_8353488 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6279801	linear	EST 16-JUL-2002
5', mRNA sequence.			
ACCESSION	BQ707318		
VERSION	BQ707318.1	GI:21846217	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1. (bases 1 to 976)		
TITLE	NIH-MGC http://mgc.nci.nih.gov/.		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)		
COMMENT	Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: rgs@nih.gov Tissue Procurement: Dr. Mark Watson CDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LICM2469 row: p column: 10 High quality sequence stop: 580.		
FEATURES	Location/Qualifiers		
source	1. 976 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:6279801" /lab_host="DH10B (phage-resistant)" /clone_lib="NIH MGC 113" /note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."		
ORIGIN			
Query Match	5.0%	Score 50.2;	DB 5; Length 976;
Best Local Similarity	58.7%	Fred. No. 0.032;	
Matches 105; Conservative	0;	Mismatches 73; Indels 1;	Gaps 1;
QY	681	AAGAGGGGGCAGGAGGGTTCAGAGGGGGCGGCGCTCAGGACGATGGAGGAGTCAGTCAGTCG	740

3.4g of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to L-one-linker Li-Sal4, purified by phenol/chloroform extraction, and separated from free linkers by Centricon-100 column. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S for 25 cycles. The products were purified by phenol/chloroform extraction and Centricon-100 column. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pCMV-SPORT6 plasmid vector. The average insert size is about 3.6kb."

ORIGIN

Query Match 5.0%; Score 50; DB 6; Length 825;
 Best Local Similarity 69.4%; Pred. No. 0.035;
 Matches 68; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

Qy 743 GCTGAAAGGAGGAGGAGGCTTCGAGCCAGCGCTTCCAGAGCTGGAAAA 802
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 Db 440 GCTGCTTGAAGGAGGAGGCTTCGAGCCAGCGGATGCGAGCACTCCAGAGCTGGAA 499
 |||||

Qy 803 AGCGGGAGGAGGAGGCTTCGAGCGAGCTTCGAGCGAGAA 840
 |||||
 Db 500 GCCAGGAAAGGAGGATCTCCCTCGAGCTTCCAGAAAGAA 537
 |||||

RESULT 8

AQ405885/c
 LOCUS AQ405885 525 bp DNA linear GSS 13-MAR-1999
 DEFINITION HS 5043 B2 P07 T7 RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plates=619 Col=14 Row=L, genomic survey sequence.
 ACCESSION AQ405885
 VERSION AQ405885.1 GI:4415873
 KEYWORDS GSS.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 525)
 AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.
 TITLE Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
 PUBMED 10449764
 COMMENT Contact: Mahairas GG, Wallace JC, Hood L
 High Throughput Sequencing Center
 University of Washington
 401 Queen Anne Avenue North, Seattle, WA 98109, USA
 Tel: (206) 616-3618
 Fax: (206) 616-3887
 Email: jwallace@u.washington.edu
 Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering.bac.htm) or from Research Genetics (info@resgen.com). BAC end Web Server: http://www.htac.washington.edu
 Plate: 619 Row: L Column: 14
 Seq primer: 77
 Class: BAC ends
 High quality sequence stop: 525.
 Location/Qualifiers
 1..525
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /clone="Plate=619 Col=14 Row=L"
 /sex="male"
 /clone_lib="RPCI-11 Human Male BAC Library"

FEATURES
source

1..525
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /clone="Plate=619 Col=14 Row=L"
 /sex="male"
 /clone_lib="RPCI-11 Human Male BAC Library"

/note="Vector: pBACE3.6; Site 1: EcoRI; Site 2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACE3.6 vector at EcoRI sites"

ORIGIN

Query Match 4.9%; Score 49.2; DB 9; Length 525;
 Best Local Similarity 59.4%; Pred. No. 0.052;
 Matches 120; Conservative 0; Mismatches 78; Indels 4; Gaps 2;

Qy 611 GTGAGGACCTCTGGAGTCTCTGGGATCTCTCGGACTTACTTCGAGGCCCGGAAAAAGTAAATCCAG 670
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 Db 317 GTGATTGGATTGAGGATCTTCAGATGAGGAGATTATCTGGGTGGCCCTAAAGTAAATCACA 258
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Qy 671 GGGTTCTGGGAGAGGCGGCGAGGAGGTCTCAGAGGGGGGCGAGCCCTCAGGAGCATGGAGGC 730
 |||||
 Db 257 GGGGTCTTATGAGACGAGGCGAGGGGTCTCAGATCTCAGACAGACTGGAAGATGC---C 201
 |||||

Qy 731 AGTCAGTCTCAGGCTGAAAAGGAGGAGGAGGCGCTTCGAGCCCGAGCCCTGCAAGC-GCCTCC 789
 |||||
 Db 200 ACCTGTTGGCTTTGAAGTGGAGAGGGGCCATGAGCCAGGCGATGCAGGCAGCTTCC 141
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Qy 790 AGAAGCTGGAAGAAAGCGGGGAA 811
 |||||
 Db 140 ACAAGCTGGAAGAAAGGAA 119
 |||||

RESULT 9

AQ112190
 LOCUS AQ112190 439 bp DNA linear GSS 29-AUG-1998
 DEFINITION CIT-HSP-2373021.TR CIT-HSP Homo sapiens genomic clone 2373021, genomic survey sequence.
 ACCESSION AQ112190
 VERSION AQ112190.1 GI:3484350
 KEYWORDS GSS.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 439)
 AUTHORS Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and Venter,J.C.
 TITLE Use of a random human BAC End Sequence Database for Sequence-Ready Map Building
 JOURNAL Unpublished (1998)
 COMMENT Other GSSs: CIT-HSP-2373021.TF
 Contact: Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: mdadams@tigr.org
 Clones are available from Research Genetics (info@resgen.com). BAC end search page:
 http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
 Seq primer: M13 Reverse
 Class: BAC ends.
 Location/Qualifiers
 1..439
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 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /clone="2373021"
 /sex="Male"
 /cell_type="Sperm"
 /clone_lib="CIT-HSP"
 /note="Vector: pBelOBAC11; Site 1: HindIII; Site 2: HindIII"

ORIGIN


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/db_xref="taxon:9913"
/clone="CH240_419J4"
/sex="Male"
/cell_type="Blood"
/clone_lib="CHORI-240"
/notes=Vector; PTARBAC1.3; Site.1: MboI; Site.2: MboI;
Hereford bull Li Domino 99375; CHORI-240 Bovine BAC
library (Male) produced by Pieter de Jong"

ORIGIN
Query Match          4.8%; Score 47.6; DB 9; Length 780;
Best Local Similarity 69.1%; Pred. No. 0.16; Indels 0; Gaps 0;
Matches 65; Conservative 0; Mismatches 29;

759 GGGCCCTCGAGCCGAGGCTCGAAGCGCTCCAGAAGCTCGAAAAGCGGGAGGACCC 818
415 GGGCCGCGAGCGAAGAAACGCTGCTGCTCTAGACACGGGAGAGGCGAGGAAGGACCC 356
819 TCACGAGCGCTGCAGCAGCAGGAGGACCGGCTGGC 852
355 TCCCCGGAGCTGCGCGCAGGAACACACAGGCTTGC 322

RESULT 12
CNS017SY
LOCUS
DEFINITION
Drosophila melanogaster genome survey sequence SP6 end of BAC
BACN37L08 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ALI08460
ALI08460.1 GI:5628764
GSS..
Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Dipera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
Genoscope.
Direct Submission
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : secre@genoscope.cns.fr)
- web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a
collaboration with the European Drosophila Genome Project (EDGP) -
http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
library (Dros BAC) was made by Alain Billaud at CEPH (Centre
d'Etude du Polymorphisme Humain) with funding provided by a MRC
project grant. The DNA was prepared from embryos by Alain Bucheton
and Genevieve Payan. It has been constructed in the vector
pBelOBAC11.

FEATURES
source          Location/Qualifiers
1..1101
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACN37L08"
/clone_lib="DrosBAC"
/plasmid="pBelOBAC11"
/note="end : SP6"

ORIGIN
Query Match          4.6%; Score 46.2; DB 10; Length 1101;
Best Local Similarity 14.0%; Pred. No. 0.41; Indels 2; Gaps 1;
Matches 41; Conservative 155; Mismatches 95;

707 GGGCAGGCTTACGACGATGGAGGAGCTCAGTCTGAGGCTGAAAAGGAGGAGGCGCTCG 766
807 GSCCGVSSCSAVSASSSVMSKVASAVASCAVASGWSAGVSSCRSSVASSVSAAS 866
767 AGCCAGGCTTG--CAGCGCCTTCAGAGCTCGAAAAGCGGGAGGACCTTCACG 824
867 VSSSVSSSSSVVSAVASASSSASSASMAVAAAASVAVSSVAVSSSSSSSSSS 926

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Db 283 AAGG 286

Search completed: January 10, 2006, 15:07:42
Job time : 4715 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 10, 2006, 11:12:13 ; Search time 210.333 Seconds
(without alignments)
3469.703 Million cell updates/sec

Title: US-09-615-039-1_COPY_9500_10500
Perfect score: 1001
Sequence: 1 aaagaccgagcattggcac.....ggattatttcaaaacaagg 1001

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4637633 seqs, 364532575 residues

Total number of hits satisfying chosen parameters: 9275266

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA New:*

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- 2: /cgn2_6/ptodata/1/pubna/US06 NEW PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubna/US07 NEW PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubna/PCT_NEW PUB.seq:*
- 5: /cgn2_6/ptodata/1/pubna/US09 NEW PUB.seq:*
- 6: /cgn2_6/ptodata/1/pubna/US10 NEW PUB.seq:*
- 7: /cgn2_6/ptodata/1/pubna/US11 NEW PUB.seq:*
- 8: /cgn2_6/ptodata/1/pubna/US11 NEW PUB.seq:*
- 9: /cgn2_6/ptodata/1/pubna/US11 NEW PUB.seq:*
- 10: /cgn2_6/ptodata/1/pubna/US60 NEW PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	61.2	6.1	191684	7	US-11-121-086-2
2	55	5.5	33737	6	US-10-276-233A-7
3	55	5.5	175100	7	US-11-121-086-21
4	49.8	5.0	1707	6	US-10-750-185-60686
5	49.8	5.0	1707	6	US-10-750-623-60686
6	45.8	4.6	203467	7	US-11-121-086-50
7	42.8	4.3	96256	6	US-10-775-189-352
8	41.2	4.1	120096	7	US-11-121-086-24
9	40.4	4.0	319608	7	US-11-145-703-1
10	39	3.9	5651	6	US-10-750-185-38240
11	39	3.9	5651	6	US-10-750-623-38240
12	38.8	3.9	191350	6	US-10-857-780-4
13	38.6	3.9	4136	7	US-11-136-527-2296
14	38.4	3.8	126552	7	US-11-121-086-1
15	38	3.8	185393	7	US-11-121-086-101
16	37.6	3.8	75007	6	US-10-995-561-13194
17	37.2	3.7	2055	6	US-10-750-185-46360
18	37.2	3.7	2055	6	US-10-750-623-46360
19	37	3.7	51749	6	US-10-995-561-13245
20	37	3.7	168516	7	US-11-121-086-3
21	36.4	3.6	175673	7	US-11-121-086-55
22	36	3.6	150468	7	US-11-112-908-56
23	36	3.6	193789	7	US-11-112-908-55

c 24	35.6	3.6	20945	6	US-10-995-561-13463	Sequence 13463, A
c 25	35.6	3.6	23082	6	US-10-995-561-13457	Sequence 13457, A
c 26	35.6	3.6	94510	6	US-10-995-561-13332	Sequence 13332, A
c 27	35.4	3.5	792	7	US-11-102-883-35	Sequence 35, Appl
c 28	35.4	3.5	825	7	US-11-102-883-33	Sequence 33, Appl
c 29	35.4	3.5	1608	6	US-10-750-185-37878	Sequence 37878, A
c 30	35.4	3.5	1608	6	US-10-750-623-37878	Sequence 37878, A
c 31	35.4	3.5	4360	7	US-11-109-157A-21	Sequence 21, Appl
c 32	35.2	3.5	40000	6	US-10-995-561-13510	Sequence 13510, A
c 33	35.2	3.5	171486	7	US-11-121-086-105	Sequence 105, App
c 34	35.2	3.5	179777	7	US-11-121-086-106	Sequence 106, App
c 35	35	3.5	79528	6	US-10-276-233A-6	Sequence 6, Appl
c 36	35	3.5	84409	6	US-10-995-561-13494	Sequence 13494, A
c 37	35	3.5	86131	6	US-10-995-561-13298	Sequence 13298, A
c 38	34.8	3.5	137935	6	US-10-995-561-13278	Sequence 13278, A
c 39	34.8	3.5	285300	6	US-10-857-780-5	Sequence 6, Appl
c 40	34.6	3.5	600	7	US-11-136-527-5440	Sequence 5440, Ap
c 41	34.6	3.5	974	7	US-11-136-527-1344	Sequence 1344, Ap
c 42	34.6	3.5	172111	7	US-11-121-086-28	Sequence 28, Appl
c 43	34.4	3.4	200628	7	US-11-121-086-62	Sequence 62, Appl
c 44	34.2	3.4	201	6	US-10-995-561-38077	Sequence 38077, A
c 45	34.2	3.4	201	6	US-10-995-561-54894	Sequence 54894, A

ALIGNMENTS

RESULT 1
US-11-121-086-2
; Sequence 2, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121.086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 191684
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-2

Query Match	6.1%	Score 61.2;	DB 7;	Length 191684;
Best Local Similarity	52.5%	Pred. No. 8.4e-08;		
Matches 191;	Conservative 0;	Mismatches 158;	Indels 15;	Gaps 2;
Qy 550	ATTCCTCCCAACCTGTGTGACAGAACCCGCGCCGAGGCGCTTTGAGGTGTGATCTC	609		
Db 113378	AATCCCTGGGACCTGTGGCCAGGCGACCTCACTCAGCCATAGACTGCAGGTGCGACTTG	113437		
Qy 610	CGTGAGGACCTGAGTCTGGGATCCTTCGGGACTACTCGCAGGCGCCGAAAGTAATCCA	669		
Db 113438	AACAAAGACCTCGAGGGTGGTGAACTTTGCACTATTCGCGGAACCCAGTGTCTCTCAC	113497		
Qy 670	GGGGTTCGGAACAGCGCGGACAGGGTTCAGAGGGGGGCGGCTCAGGACGATGGAGG	729		
Db 113498	AGGTTCCTTTAAGAGGAGGCGAGGGTGTGAGTGTGAGAGACTGAGAAAGGCTGTGC	113557		
Qy 730	CAGTCAGTCTGAGGCTGAAAGAGGAGGAGGGGCTTCGAGCCGAGGCTTCGAAAGCGCTCC	789		
Db 113558	-----TGTGGTTCGAGGAGGAGGAGGCGGCTTCGAGGAGGAGTGCAGGTGCGCTCC	113610		
Qy 790	AGAGCTGGAAAAAGCGGGAGGAGGACCTTCACGAGGCTTCGAGCAGG-----AAG	841		
Db 113611	AGATGCTGGAAAGCGGGCACTGACTCTCCCGAGGCTTCGGGAGGCGCCAGTCTGTC	113670		
Qy 842	GCACGGCTGGCCCTTAGCCACCAGGGGCCATCGTGGACCTCCGCGCTCCGTCATAGG	901		

Db 113671 CCACAGCTTGACTTGAGCCAGCAGGCTGACTTTGGACTTCCAGCCAGCGCTGAGAG 113730
Qy 902 AGGG 905
Db 113731 AGAG 113734

RESULT 2
US-10-276-233A-7/c
; Sequence 7, Application US/10276233A
; Publication No. US20050260572A1
; GENERAL INFORMATION:
; APPLICANT: Hitachi Software Engineering Co., Ltd.
; TITLE OF INVENTION: A method of predicting cancer condition
; FILE REFERENCE: PH-1533-PCT
; CURRENT APPLICATION NUMBER: US/10/276,233A
; PRIOR FILING DATE: 2002-11-14
; PRIOR FILING DATE: 2001-03-14
; PRIOR FILING DATE: 2001-03-14
; PRIOR FILING DATE: 2001-04-06
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 7
; LENGTH: 33737
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-276-233A-7

Query Match 5.5%; Score 55; DB 6; Length 33737;
Best Local Similarity 54.1%; Pred. No. 3.1e-06;
Matches 112; Conservative 0; Mismatches 95; Indels 0; Gaps 0;
Qy 555 CCCAAACCTGTGGACAGAACCCGCCGCCAGGCGCTTTGGCAGGTGTGATCTCCGTGA 614
Db 33347 CCTGGACCTGTCTATGTGTATGTGTGGCCACAGGACTTTGCAGATGTCAATTA 33288
Qy 615 GGACCCCTGAGGTCTGGGATCTTCGGGACTACCTGCAGGCCCGAAAAAGTAATCCAGGGGT 674
Db 33287 GGAGCCTGAGGTGGCAAAATGCTCTCGGGTTATCCAGTGGCTCCAGCTGGGGTCTTTAT 33228
Qy 675 TCTGGGAAGAGCGGGCAGAGGGTTCAGAGGGGGCAGCCTCAGGACGATGGAGGCGATC 734
Db 33227 AGAAGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 33168
Qy 735 AGTCTGAGGCTGAAAGAGGAGGAGGAGG 761
Db 33167 ACGGAGAGAGAGAGAGAGAGAGAGG 33141

RESULT 3
US-11-121-086-21/c
; Sequence 21, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT FILING DATE: 2005-05-04
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 21
; LENGTH: 175100
; TYPE: DNA
; ORGANISM: Homo sapiens

US-11-121-086-21
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Best Local Similarity 54.1%; Pred. No. 6.8e-06;
Matches 112; Conservative 0; Mismatches 95; Indels 0; Gaps 0;
Qy 555 CCCAAACCTGTGGACAGAACCCGCCGCCAGGCGCTTTGGCAGGTGTGATCTCCGTGA 614
Db 86852 CCTGGACCTGTCTATGTGTATGTGTGGCCACAGGACTTTGCAGATGTCAATTA 86793
Qy 615 GGACCCCTGAGGTCTGGGATCTTCGGGACTACCTGCAGGCCCGAAAAAGTAATCCAGGGGT 674
Db 86792 GGAGCCTGAGGTGGGAAATGCTCTCGGGTTATCCAGGTGGGTCCAAGCTGGGGTCTTTAT 86733
Qy 675 TCTGGGAAGAGCGGGCAGAGGGTTCAGAGGGGGCAGCCTCAGGACGATGGAGGCGATC 734
Db 86732 AGAAGAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 86673
Qy 735 AGTCTGAGGCTGAAAGAGGAGGAGGAGG 761
Db 86672 ACGGAGAGAGAGAGAGAGAGAGAGAGG 86646

RESULT 4
US-10-750-185-60686
; Sequence 60686, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; PRIOR FILING DATE: 2003-12-31
; PRIOR FILING DATE: 2003-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 60686
; LENGTH: 1707
; TYPE: DNA
; ORGANISM: Bovine 19866881589878
US-10-750-185-60686

Query Match 5.0%; Score 49.8; DB 6; Length 1707;
Best Local Similarity 53.3%; Pred. No. 3.1e-05;
Matches 105; Conservative 0; Mismatches 92; Indels 0; Gaps 0;
Qy 616 GACCCCTGAGGTCTGGGATCTTCGGGACTACCTGCAGGCCCGAAAAAGTAATCCAGGGGT 675
Db 1428 GGCCTTGAGATGGAGACTCTGTAGATTATCCAGGAGGGGCCCAAGCAATCAGAGGGT 1487
Qy 676 CTGGGAAGAGCGGGCAGGAGGGTTCAGAGGGGGCAGCCTCAGGACGATGGAGGCGATCA 735
Db 1488 CCTTAGAAGTCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1547
Qy 736 GTCTGAGGCTGAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 795
Db 1548 TGCTGGCTTTGAGATGTGGGAAGGGGCCCAAGCAAGGAGGAGGAGGAGGAGGAGGAGGAG 1607
Qy 796 TGGAAAAAGCGGGGAG 812
Db 1608 TGGAAAAAGCGGGGAG 1624
RESULT 5
US-10-750-623-60686
; Sequence 60686, Application US/10750623

OTHER INFORMATION: exon Q1 complement g34872 gene
FEATURE:
NAME/KEY: exon
LOCATION: 229647..229742
OTHER INFORMATION: exon X complement g34872 gene
FEATURE:
NAME/KEY: exon
LOCATION: 230408..230721
OTHER INFORMATION: exon P complement g34872 gene
FEATURE:
NAME/KEY: exon
LOCATION: 231272..231412
OTHER INFORMATION: exon Obis complement g34872 gene
FEATURE:
NAME/KEY: exon
LOCATION: 231787..231880
OTHER INFORMATION: exon O2 complement g34872 gene
FEATURE:
NAME/KEY: exon
LOCATION: 231870..231879
OTHER INFORMATION: exon O1 complement g34872 gene
FEATURE:
NAME/KEY: exon
LOCATION: 234174..234321
OTHER INFORMATION: exon O complement g34872 gene
FEATURE:
NAME/KEY: exon
LOCATION: 237406..237428
OTHER INFORMATION: exon Nbis complement g34872 gene
FEATURE:
NAME/KEY: exon
LOCATION: 239719..239807
OTHER INFORMATION: exon N2 complement g34872 gene
FEATURE:
NAME/KEY: exon
LOCATION: 239719..239853
OTHER INFORMATION: exon N complement g34872 gene
FEATURE:
NAME/KEY: exon
LOCATION: 240528..240569
OTHER INFORMATION: exon M1117 complement g34872 gene
FEATURE:
NAME/KEY: exon
LOCATION: 240528..240596
OTHER INFORMATION: exon M1090 complement g34872 gene
FEATURE:
NAME/KEY: exon
LOCATION: 240528..240617
OTHER INFORMATION: exon M1069 complement g34872 gene
FEATURE:
NAME/KEY: exon
LOCATION: 240528..240644
OTHER INFORMATION: exon MS2 complement g34872 gene
FEATURE:
NAME/KEY: exon
LOCATION: 240528..240824
OTHER INFORMATION: exon M862 complement g34872 gene
FEATURE:
NAME/KEY: exon
LOCATION: 240528..240994
OTHER INFORMATION: exon M692 complement g34872 gene
FEATURE:
NAME/KEY: exon
LOCATION: 240528..241685
OTHER INFORMATION: exon M1 complement g34872 gene
FEATURE:
NAME/KEY: exon
LOCATION: 240800..240993
OTHER INFORMATION: exon MS1 complement g34872 gene
FEATURE:
NAME/KEY: misc feature
LOCATION: 241686..243685
OTHER INFORMATION: 5 regulatory region g34872 gene

FEATURE:
NAME/KEY: misc feature
LOCATION: 290652..292652
OTHER INFORMATION: 3'regulatory region g34665 gene
Query Match 4.0%; Score 40.4; DB 7; Length 319608;
Best Local Similarity 60.2%; Pred. No. 0.31;
Matches 100; Conservative 1; Mismatches 62; Indels 3; Gaps 2;
Qy 694 GAGGGTCAGAGGGGGGCGAGCTCAGGACGATGGAGGAGTCAGTCTCAGGGCTGAAAGGG 753
Db 238738 GAGAGGGGGATGCTGGGAAGAAGAGTGTCTCAGAGAAGCAACATTGCTGACTCTAAGACAG 238797
Qy 754 AGGGAGGGCTCGAGGCCAGGCCCTGCAAG-CGCTCCAGAAAGCTGGAAGAGC--GGGGA 810
Db 238798 AGGCGAGCCACGAGCCAGGCATGCAAGAGGCTCCAGAAAGCTGGGCGAGCAAGAGAA 238857
Qy 811 AGGAGCCCTCAGAGGAGCTTCAGAGCAAGAGGACGGCTGGCCCTT 856
Db 238858 TGGACTCAGCCCTGGAGCCTCCAGAAGGCATGCAGCCCTGCCATT 238903
RESULT 10
US-10-750-185-38240
; Sequence 38240, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; PRIOR FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38240
; LENGTH: 5651
; TYPE: DNA
; ORGANISM: Bovine 19866880256159
US-10-750-185-38240
Query Match 3.9%; Score 39; DB 6; Length 5651;
Best Local Similarity 57.1%; Pred. No. 0.12;
Matches 109; Conservative 0; Mismatches 80; Indels 2; Gaps 2;
Qy 517 GCAGGATAATGCTCTAGAGATGCCACGTCCTGATTTCCCAACC-TGTGGACAGAAC 575
Db 1690 GCAGGACAACTCCAGAGATGTCCCTCTCTGATCCCGCCCAAGAGAGCGCGCC 1749
Qy 576 GCGCGGCGCCAGGGCTTTCAGGTGTGATCTCGTGAGGACCTGAGGTCTGGATCC 635
Db 1750 CGACAAGACAAAGGGCTTCGGGGTGTGATTAGTGACA-GACCTGAGATGGGAGCA 1808
Qy 636 TTGGGGACTACTCGAGCGCCGAAAGTAATCCAGGGGTCTCGGAAGAGCGCGGCGAGA 695
Db 1809 GTCCCGATTGCTGGGTGGCCCGCTGCATCACCAGGGTCTTGAAAACAGCGCGGGGG 1868
Qy 696 GGGTCAGAGGG 706
Db 1869 GGCACGGAGGG 1879
RESULT 11
US-10-750-623-38240
; Sequence 38240, Application US/10750623
; Publication No. US20050287531A1

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; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38240
; LENGTH: 5651
; TYPE: DNA
; ORGANISM: Bovine 19866880256159
; US-10-750-623-38240

Query Match          3.9%; Score 39; DB 6; Length 5651;
Best Local Similarity 57.1%; Pred. No. 0.12;
Matches 109; Conservative 0; Mismatches 80; Indels 2; Gaps 2;

Qy 517 GCAGGATAAGTCTTAGAGATGCCACGTCCTGATTCCCCAAACC-TGTGGACAGAACCC 575
    |||||
Db 1690 GCAGGACAAGTCTCCAGAGATGTCCTCTCTGATGCCAGGCCCAAGAGAGACCGCGCC 1749

Qy 576 CGCCCGGCCCGAGGCTTTTCAGGTGTGATCTCGTGAGGACCTCAGGTCTGGGATCC 635
    |||||
Db 1750 CGACAAGACAAAGGGCTTCGGGGTGTGATTAGTGACA-GACCTCAGATGGGACATT 1808

Qy 636 TTCGGGACTACTCTCAGCGCCGAAAGTAATCCAGGGGTTCTGGGAAGAGCGCGGCAGGA 695
    |||||
Db 1809 GTCCCGATTGCTGGGTGGCCCGTGCCATCACCAGGCTCTGAAACAGCGCGGGGGCG 1868

Qy 696 GGGTCAGAGGG 706
    |||||
Db 1869 GGCACGGAGGG 1879

RESULT 12
US-10-857-780-4/c
; Sequence 4, Application US/10857780
; Publication No. US20050272043A1
; GENERAL INFORMATION:
; APPLICANT: ROTH, RICHARD B.
; APPLICANT: BRAUN, ANDREAS
; APPLICANT: KAMMERER, STEFAN M.
; APPLICANT: NELSON, MATTHEW ROBERTS
; APPLICANT: RENELAND, RIKARD HENRY
; APPLICANT: HOVAL-WRIGHTSON, CAROLYN R.
; TITLE OF INVENTION: METHODS FOR IDENTIFYING RISK OF BREAST CANCER AND TREATMENTS
; FILE REFERENCE: THEREOF
; FILE REFERENCE: SEQ-4069-CP
; CURRENT APPLICATION NUMBER: US/10/857,780
; CURRENT FILING DATE: 2004-05-28
; PRIOR APPLICATION NUMBER: 10/723,681
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: 60/490,234
; PRIOR FILING DATE: 2003-07-24
; PRIOR APPLICATION NUMBER: 60/525,239
; PRIOR FILING DATE: 2003-11-25
; NUMBER OF SEQ ID NOS: 4962
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 191350
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature

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; LOCATION: (16914)..(16914)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (19266)..(19266)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (26334)..(26334)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (34457)..(34472)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (38627)..(38628)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (40555)..(40555)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (57355)..(57355)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (61207)..(61207)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (64980)..(64980)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (64987)..(64987)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (81452)..(81452)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (95893)..(95893)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (103359)..(103359)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (117565)..(117565)
; OTHER INFORMATION: n is a, c, g, or t
; US-10-857-780-4

Query Match          3.9%; Score 38.8; DB 6; Length 191350;
Best Local Similarity 51.4%; Pred. No. 0.75;
Matches 142; Conservative 0; Mismatches 127; Indels 7; Gaps 2;

Qy 537 TGCCACGTCCTGATTCCTCCCAACCTGTGGACAGACCCCGCGGCCCGAGGGCCTTTG 596
    |||||
Db 140402 TGTCCACGTCCTTAATCTCTGGAACATCTGAATGCTACTTTATATGGCAAAAGGACITTTG 140343

Qy 597 CAGGTGTGATCTCCGTGAGGACCTCAGGCTCTGG-GATCCTTCGGGACTACCTCGAGGCC 655
    |||||
Db 140342 CAAATGTGATTAAGAAATGGTCTTGAGATGGGAGATGATCCTGGATTTTCTGAATGGA 140283

Qy 656 CGAAAGTAATCCAGGGGTTCTGGGAAGAGCGCGGCGAGGAGGTTCAGAGGGGGCAGCCT 715
    |||||
Db 140282 CTTGATGTAATCCTGATGCGAGGGAGCGGAGGCTCAGAGAGAGTAGTAG-----GACA 140229

Qy 716 CAGGACGATGGAGCGACTCAGTCTGAGGCTGMAAAGGAGGAGGGGCTCGAGCCAGGC 775

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Db 140228 CATAAAGGTGGAAACAAGAGGTTAGAGGGACACAAAGGAAGGGAGGCCACCAGGCCAGGCA 140169
Qy 776 CTGCAAGCGCTCCAGAGCTGGAAAAGCGGGAA 811
Db 140168 TGCAGGTGGCTTCTGGAAAGCTGGAAAAGCGCAAGGAA 140133

RESULT 13

US-11-136-527-2296
; Sequence 2296, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2296
; LENGTH: 4136
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-2296

Query Match 3.9%; Score 38.6; DB 7; Length 4136;
Best Local Similarity 56.8%; Pred. No. 0.14;
Matches 71; Conservative 0; Mismatches 54; Indels 0; Gaps 0;
Qy 676 CTGGGAAGCGCGGCGAGGGTTCAGAGGGGGCGCCTCAGGACGATGAGGCGCTCA 735
Db 71 CAGGAAGCACGACGCGGGGAGCAGGCAAGGGGGCGAGCGCCCGGGCCGCGCAAGTGGCC 130
Qy 736 GTCTGAGGCTGAAAAGGAGGAGGGCTTCAGAGCCAGGCTGCAAGCGCCTCCAGGAAGC 795
Db 131 GTCAAGGGTCTGCGGGGAGGAGCTAGCTTGACCCAGGCGACCAAGGGAACCTTCAGACGG 190
Qy 796 TGGAA 800
Db 191 TAGCA 195

RESULT 14

US-11-121-086-1/c
; Sequence 1, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 126552
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-1

Query Match 3.8%; Score 38.4; DB 7; Length 126552;
Best Local Similarity 65.7%; Pred. No. 0.82; Mismatches 36; Indels 1; Gaps 1;
Matches 71; Conservative 0;
Qy 734 CAGTCTGAGGCTGAAAAGGAGGAGGGCTTCAGCCAGGCGCTCGAAGCGCCTCCAGAA 793

Db 69519 CACTGTGGCTGTGAAGGGGGAGAAAGGCCCTTAAGATGAGGGATGCGGACGCCCTCTAGAC 69460
Qy 794 GCTGGAAAAGCGGGGAAGGAGCCCTCCAC-GGAGCCTGCAGCAGGAA 840
Db 69459 CTTGGGNAAGCAGGAATGGGTTCTCCCTGGAGCTCCAGGAGGGA 69412

RESULT 15

US-11-121-086-101/c
; Sequence 101, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 101
; LENGTH: 185393
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-101

Query Match 3.8%; Score 38; DB 7; Length 185393;
Best Local Similarity 60.8%; Pred. No. 1.3;
Matches 79; Conservative 0; Mismatches 50; Indels 1; Gaps 1;
Qy 576 CGCCCGCGCCCGCAGGGCCTTTGCGAGGTGTGATCTCCGTGAGGACCCCTGAGGTCTGGGATCC 635
Db 116833 CACATGSCAAAAGCGAGTTTGCAGATGTGATTTAATTCAGTATCTTGAGATAGGAGACA 116774
Qy 636 TTGCGGACTACCTGTCAGGCGCCGAAAAGTAATC-CAGGGGTTCTGGGAAGAGCGCGGCGAGG 694
Db 116773 TCTTGGATTACCCAGATGGACCCAAAGGAATCACAAAGGCTTCTTCAAGAGAGAAACAGA 116714
Qy 695 AGGCTCAGAG 704
Db 116713 AGAGTCAGAG 116704

Search completed: January 10, 2006, 20:45:46
Job time : 213.333 secs

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Db 7349 TACAAGACGGGAAATCCCTGCTAAATATGCTTTTAAACAACTGGTTTAAACAAACGGGTC 7408
Qy 181 CATCCGACCGGTGACAGTTCTCTACAGTGAAGAGGAACATGCGCTTTTATAAAGCCCTGCA 240
Db 7409 CATCCGACCGGTGACAGTTCTCTACAGTGAAGAGGAACATGCGCTTTTATAAAGCCCTGCA 7468
Qy 241 GGCATCTCAAGGGAATTTACGCTGAGTCAAACTGCCACCTCCATGGGATACGTACGCAAC 300
Db 7469 GGCATCTCAAGGGAATTTACGCTGAGTCAAACTGCCACCTCCATGGGATACGTACGCAAC 7528
Qy 301 ATGCTCAAAAAGAAAGAAATTTCAACCCATGCGAGGAGTGGTT-GGGGGGTTTAAAGACG 359
Db 7529 ATGCTCAAAAAGAAAGAAATTTCAACCCATGCGAGGAGTGGTTTAAAGGCGTTTAAAGACG 7588
Qy 360 GTGGGGCAGCAGTGGGGCTACTGACGACCTTTTACTAAAGCCAGTTTCTGTGTTTC 419
Db 7589 GTGGGGCAGCAGTGGGGCTACTGACGACCTTTTACTAAAGCCAGTTTCTGTGTTTC 7648
Qy 420 TGATGGTATTGGCTCAGTTATGGGAGACTAAACATAGGAGTGGGATGGGGGAACCCG 479
Db 7649 TGATGGTATTGGCTCAGTTATGGGAGACTAAACATAGGAGTGGGATGGGGGAACCCG 7708
Qy 480 GAGCTGTGCCATCTTTGCCATGCCAGTGTCTCTGGGCAAGATATGCTCTAGAGATGC 539
Db 7709 GAGCTGTGCCATCTTTGCCATGCCAGTGTCTCTGGGCAAGATATGCTCTAGAGATGC 7768
Qy 540 CCAGTCTGATTTCCCTGAGGACCTCAGGTCGGAAGAACCCGCGCGCCAGGGCCCTTTGCAG 599
Db 7769 CCAGTCTGATTTCCCTGAGGACCTCAGGTCGGAAGAACCCGCGCGCCAGGGCCCTTTGCAG 7828
Qy 600 GTGTGATCTCCGTGAGGACCTCAGGTCGGAAGAACCCGCGCGCCAGGGCCCTTTGCAG 659
Db 7829 GTGTGATCTCCGTGAGGACCTCAGGTCGGAAGAACCCGCGCGCCAGGGCCCTTTGCAG 7888
Qy 660 AAGTAATCCAGGGGTTCTGGGAAGAGCGCGGCAAGAGGTCAGAGGGGGGAGGCTCAGG 719
Db 7889 AAGTAATCCAGGGGTTCTGGGAAGAGCGCGGCAAGAGGTCAGAGGGGGGAGGCTCAGG 7948
Qy 720 ACCATGGAGGCACTCAGTCTGAGCTGAGGTCAGAAAGAGGAGGAGGCTCCAGCCCTGC 779
Db 7949 ACCATGGAGGCACTCAGTCTGAGCTGAGGTCAGAAAGAGGAGGAGGCTCCAGCCCTGC 8008
Qy 780 AAGCGCTCCAGAGCTGGAAGAACCGGGAGAGGACCTCCAGAGGCTTCAGCAGGGA 839
Db 8009 AAGCGCTCCAGAGCTGGAAGAACCGGGAGAGGACCTCCAGAGGCTTCAGCAGGGA 8068
Qy 840 AGGCAGGCTGGCCCTTTAGCCCAACAGGCGCCATCGTGGACCTCCGCGCTCCGTCCTATA 899
Db 8069 AGGCAGGCTGGCCCTTTAGCCCAACAGGCGCCATCGTGGACCTCCGCGCTCCGTCCTATA 8128
Qy 900 GGAGGGCACTCGGCTGCCCTTTAGCATGAGTGTGTGGGATTTGCAAGCAACAGG 959
Db 8129 GGAGGGCACTCGGCTGCCCTTTAGCATGAGTGTGTGGGATTTGCAAGCAACAGG 8188
Qy 960 AAACCCATGCACTGTGAATCTAGGATTTTCAAAAACAAAGG 1001
Db 8189 AAACCCATGCACTGTGAATCTAGGATTTTCAAAAACAAAGG 8230

RESULT 11

US-10-840-455-43
; Sequence 43, Application US/10840455
; Publication No. US20050032094A1
; GENERAL INFORMATION:
; APPLICANT: Bayer Aktiengesellschaft
; APPLICANT: Hagen, Gustav
; APPLICANT: Wick, Maresa
; APPLICANT: Zubov, Dmitry
; TITLE OF INVENTION: Regulatory DNA Sequences of the Gene for the Human Catalytic
; FILE OF INVENTION: Telomerase Subunit, and Their Diagnostic and Therapeutic Use
; FILE REFERENCE: Lea 32 805C1
; CURRENT APPLICATION NUMBER: US/10/840,455
; CURRENT FILING DATE: 2004-05-06

; PRIOR APPLICATION NUMBER: PCT/EP98/08216
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: US 09/582,246
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: DE19757984.1
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43
; LENGTH: 26414
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-840-455-43

Query Match 98.7%; Score 988.4; DB 8; Length 26414;
Best Local Similarity 99.8%; Pred. No. 1.1e-312;
Matches 1000; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
Qy 1 AAAGAGACCCAGCATTTGGCACCCCTGGACATTTGCCCCACAGCCCTGGGAATTCACGTGAC 60
Db 7229 AAAGAGACCCAGCATTTGGCACCCCTGGACATTTGCCCCACAGCCCTGGGAATTCACGTGAC 7288
Qy 61 TAGCGACATCATGTACACATCTCCCGTCCACGACCGACCCCGCTGTTTATTTTAAATAGC 120
Db 7289 TAGCGACATCATGTACACATCTCCCGTCCACGACCGACCCCGCTGTTTATTTTAAATAGC 7348
Qy 121 TACAAAGACGGGAAATTCCTCTGCTTAAATGTCCTTTTAAACAACTGGTTTAAACAAACGGGTC 180
Db 7349 TACAAAGACGGGAAATTCCTCTGCTTAAATGTCCTTTTAAACAACTGGTTTAAACAAACGGGTC 7408
Qy 181 CATCCGACCGGTGACAGTTCTCTACAGTGAAGAGGAACATGCGCTTTTATAAAGCCCTGCA 240
Db 7409 CATCCGACCGGTGACAGTTCTCTACAGTGAAGAGGAACATGCGCTTTTATAAAGCCCTGCA 7468
Qy 241 GGCATCTCAAGGGAATTTACGCTGAGTCAAACTGCCACCTCCATGGGATAGTACGCAAC 300
Db 7469 GGCATCTCAAGGGAATTTACGCTGAGTCAAACTGCCACCTCCATGGGATAGTACGCAAC 7528
Qy 301 ATGCTCAAAAAGAAAGAAATTTCAACCCATGCGAGGAGTGGTT-GGGGGGTTTAAAGACG 359
Db 7529 ATGCTCAAAAAGAAAGAAATTTCAACCCATGCGAGGAGTGGTTTAAAGGCGTTTAAAGACG 7588
Qy 360 GTGGGGCAGCAGTGGGGCTACTGACGACCTTTTACTAAAGCCAGTTTCTGTGTTTC 419
Db 7589 GTGGGGCAGCAGTGGGGCTACTGACGACCTTTTACTAAAGCCAGTTTCTGTGTTTC 7648
Qy 420 TGATGGTATTGGCTCAGTTATGGGAGACTAAACATAGGAGTGGGATGGGGGAACCCG 479
Db 7649 TGATGGTATTGGCTCAGTTATGGGAGACTAAACATAGGAGTGGGATGGGGGAACCCG 7708
Qy 480 GAGCTGTGCCATCTTTGCCATGCCAGTGTCTCTGGGCAAGATATGCTCTAGAGATGC 539
Db 7709 GAGCTGTGCCATCTTTGCCATGCCAGTGTCTCTGGGCAAGATATGCTCTAGAGATGC 7768
Qy 540 CCAGTCTGATTTCCCTGAGGACCTCAGGTCGGAAGAACCCGCGCGCCAGGGCCCTTTGCAG 599
Db 7769 CCAGTCTGATTTCCCTGAGGACCTCAGGTCGGAAGAACCCGCGCGCCAGGGCCCTTTGCAG 7828
Qy 600 GTGTGATCTCCGTGAGGACCTCAGGTCGGAAGAACCCGCGCGCCAGGGCCCTTTGCAG 659
Db 7829 GTGTGATCTCCGTGAGGACCTCAGGTCGGAAGAACCCGCGCGCCAGGGCCCTTTGCAG 7888
Qy 660 AAGTAATCCAGGGGTTCTGGGAAGAGCGCGGCAAGAGGTCAGAGGGGGGAGGCTCAGG 719
Db 7889 AAGTAATCCAGGGGTTCTGGGAAGAGCGCGGCAAGAGGTCAGAGGGGGGAGGCTCAGG 7948
Qy 720 ACCATGGAGGCACTCAGTCTGAGCTGAGGTCAGAAAGAGGAGGAGGCTCCAGCCCTGC 779
Db 7949 ACCATGGAGGCACTCAGTCTGAGCTGAGGTCAGAAAGAGGAGGAGGCTCCAGCCCTGC 8008
Qy 780 AAGCGCTCCAGAGCTGGAAGAACCGGGAGAGGACCTCCAGAGGCTTCAGCAGGGA 839
Db 8009 AAGCGCTCCAGAGCTGGAAGAACCGGGAGAGGACCTCCAGAGGCTTCAGCAGGGA 8068
Qy 840 AGGCAGGCTGGCCCTTTAGCCCAACAGGCGCCATCGTGGACCTCCGCGCTCCGTCCTATA 899
Db 8069 AGGCAGGCTGGCCCTTTAGCCCAACAGGCGCCATCGTGGACCTCCGCGCTCCGTCCTATA 8128
Qy 900 GGAGGGCACTCGGCTGCCCTTTAGCATGAGTGTGTGGGATTTGCAAGCAACAGG 959
Db 8129 GGAGGGCACTCGGCTGCCCTTTAGCATGAGTGTGTGGGATTTGCAAGCAACAGG 8188
Qy 960 AAACCCATGCACTGTGAATCTAGGATTTTCAAAAACAAAGG 1001
Db 8189 AAACCCATGCACTGTGAATCTAGGATTTTCAAAAACAAAGG 8230

Qy	840	AGGCA CGGCTGGGCCCTTAGCCCA CCAAGGCCCATCTGTGACCTTCGGCCTCCGTGCCATA	899
Db	8069	AGGCACGGCTGGGCCCTTAGCCCA CCAAGGCCCATCTGTGACCTTCGGCCTCCGTGCCATA	8128
Qy	900	GGAGGGCACTCGCGCTCCCTTCTAGCATCAAGTGTGTGGGATTTCAGAACGCAACAGG	959
Db	8129	GGAGGGCACTCGCGCTCCCTTCTAGCATCAAGTGTGTGGGATTTCAGAACGCAACAGG	8188
Qy	960	AAACCCATGCACGTGTAATCTAGGATTATTTCAAAACAAAGG	1001
Db	8189	AAACCCATGCACGTGTAATCTAGGATTATTTCAAAACAAAGG	8230

RESULT, T 12

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US-09-733-294A-30
; Sequence 30, Application US/09733294A
; Patent No. US2002004588A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: William Gaarde
; APPLICANT: Susan M. Freier
; APPLICANT: Edward V. Wancewicz
; TITLE OF INVENTION: ANTISENSE MODULATION OF TEXT EXPRESSION
; FILE REFERENCE: ISPH-0527
; CURRENT APPLICATION NUMBER: US/09/733,294A
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 09/572,423
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 108
; SEQ ID NO 30

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494	Qy	TTTTGCCATGCCGAGTGTCTCGGCGAGGATTAATGCTCTAGAGATGCCACGCTCCTGATTC	553
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554	Qy	CCCCAAACCTGTGGACAGAAACCCGCCGCCAGGGCCTTTGCAGGTGTGATCTCCGTG	613
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RESULT 14
US-10-027-632-134480
; Sequence 134480, Application US/10027632
; Publication No. US20020190371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 134480
; LENGTH: 683
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-134480

Query Match          62.5%;      Score 625.6;  DB 5;      Length 683;
Best Local Similarity 99.8%;      Pred. No. 3.4e-194;
Matches 625;  Conservative 1;  Mismatches 0;  Indels 0;  Gaps 0;

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QY	376	GGGGCTACTGCA CGCA CTTT TTA CTAAAGCCAGTTTCTGGTTCGTGATGGTATTTGGCTCA	435
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QY	436	GTTATGGGAGCTAACCATAGGGGAGTGGGGATGGGGAAACCCGGAGGCTGTGCCATCTT	495
DB	61	GTTATGGGAGCTAACCATAGGGGAGTGGGGATGGGGAAACCCGGAGGCTGTGCCATCTT	120
QY	496	TGCCATGCCCAGTGTCTCTGGGCAGGATAATGCTCTAGAGATGCCCAAGCTCTGATTCOC	555
DB	121	TGCCATGCCCAGTGTCTCTGGGCAGGATAATGCTCTAGAGATGCCCAAGCTCTGATTCOC	180
QY	556	CCAAACCTGTGGACAGAAACCCGCCGGCCCAAGGCTTTTGACGTGTGATCTCCGTGAG	615
DB	181	CCAAACCTGTGGACAGAAACCCGCCGGCCCAAGGCTTTTGACGTGTGATCTCCGTGAG	240
QY	616	GACCTTGAGGTCTGGGATCTTTCGGACTACCTTGACGCCCGAAGTAATCCAGGGGTT	675
DB	241	GACCTTGAGGTCTGGGATCTTTCGGGACTACCTTGACGCCCGAAGTAATCCAGGGGTT	300
QY	676	CTGGGAGAGCGGCGAGGAGGCTCAGAGGGGGGAGCCTCAGGACGATGGAGGAGATCA	735
DB	301	CTGGGAGAGCGGCGAGGAGGCTCAGAGGGGGGAGCCTCAGGACGATGGAGGAGATCA	360
QY	736	GTCTGAGGCTGAAAGGGAGGAGGGCCCTCGAGCCCGAGCCCTGCAAGGCCCTCCAGAAGC	795
DB	361	GTCTGAGGCTGAAAGGGAGGAGGGCCCTCGAGCCCGAGCCCTGCAAGGCCCTCCAGAAGC	420
QY	796	TGGAAAAAGCGGGAGAGGGAACCTTCCAAGGAGCTGACAGAGAGGACGGCTGGCCCT	855
DB	421	TGGAAAAAGCGGGAGAGGGAACCTTCCAAGGAGCTGACAGAGAGGACGGCTGGCCCT	480
QY	856	TAGCCCAACAGGGCCATCGTGGACCTCCGGCTCCGTGGCCATAGAGGGGCACTCGCGT	915
DB	481	TAGCCCAACAGGGCCATCGTGGACCTCCGGCTCCGTGGCCATAGAGGGGCACTCGCGT	540
QY	916	GCCCTTCTAGCATGAAGTGTGTGGGGATTGTGAGGAAGCAACAGGAAACCATGCACTGTG	975
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QY	976	AATCTAGGATTATTTCAAAAAACAAGG	1001
DB	601	AATCTAGGATTATTTCAAAAAACAAGG	626

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RESULT 15
US-10-027-632-134480
; Sequence 134480, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMORPHISMS IN THE HUMAN GENOME
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027.632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0

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; SEQ ID NO 134480
; LENGTH: 683
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-134480

Query Match      62.5%; Score 625.6; DB 6; Length 683;
Best Local Similarity 99.8%; Pred. No. 3.4e-194;
Matches 625; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 376 GGGGCTACTGCGACGACCTTTTACTAAAGCCAGTTCTCTGGTTCTGATGGTATTGGCTCA 435
Db 1 GGGGCTACTGCGACGACCTTTTACTAAAGCCAGTTCTCTGGTTCTGATGGTATTGGCTCA 60
QY 436 GTTATGGGAGACTAAACATAGGGAGTGGGGATGGGGAAACCCGGAGGCTGTGCCATCTT 495
Db 61 GTTATGGGAGACTAAACATAGGGAGTGGGGATGGGGAAACCCGGAGGCTGTGCCATCTT 120
QY 496 TGCATGCCCGAGTGTCTCTGGGAGGATAATGCTCTAGAGATGCCACGCTCTGATTCCC 555
Db 121 TGCATGCCCGAGTGTCTCTGGGAGGATAATGCTCTAGAGATGCCACGCTCTGATTCCC 180
QY 556 CCMAACCTGTGGACAGAACCCGCCGCCGCCAGGGCTTTGACGTTGATCTCCGTGAG 615
Db 181 CCMAACCTGTGGACAGAACCCGCCGCCGCCAGGGCTTTGACGTTGATCTCCGTGAG 240
QY 616 GACCTTGAGGTCTTGGGATCCTTCGGGACTACCTGCAGGCCCGAAAGTAATCCAGGGGTT 675
Db 241 GACCTTGAGGTCTTGGGATCCTTCGGGACTACCTGCAGGCCCGAAAGTAATCCAGGGGTT 300
QY 676 CTGGGAAGAGCGCGGCGAGAGGGTTCAGAGGGGGGAGCCTCAGGACGATGGAGGCAGTCA 735
Db 301 CTGGGAAGAGCGCGGCGAGAGGGTTCAGAGGGGGGAGCCTCAGGACGATGGAGGCAGTCA 360
QY 736 GTCTGAGGCTGAAAAGGGAGGAGGGCTTCGAGCCGAGGCCCTGCAAGGCCCTCCAGAAGC 795
Db 361 GTCTGAGGCTGAAAAGGGAGGAGGGCTTCGAGCCGAGGCCCTGCAAGGCCCTCCAGAAGC 420
QY 796 TGGMAAAGCGGGGAGGAGCCCTCCACGAGCCTGCAGCAGGAAGGCACGGCTGGCCCT 855
Db 421 TGGMAAAGCGGGGAGGAGCCCTCCACGAGCCTGCAGCAGGAAGGCACGGCTGGCCCT 480
QY 856 TAGCCACCCAGGGCCCATCGTGGACCTCCGGGCTCCGTGCCATAGGAGGGCACTCGCGCT 915
Db 481 TAGCCACCCAGGGCCCATCGTGGACCTCCGGGCTCCGTGCCATAGGAGGGCACTCGCGCT 540
QY 916 GCCCTTCTAGCATGAAAGTGTGTGGGATTTGAGAGCAACAGGAAACCCATGCACTGTG 975
Db 541 GCCCTTCTAGCATGAAAGTGTGTGGGATTTGAGAGCAACAGGAAACCCATGCACTGTG 600
QY 976 AATCTAGGATTTTCAAAACAAAGG 1001
Db 601 AATCTAGGATTTTCAAAACAAAGG 626
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Search completed: January 10, 2006, 20:35:08
Job time : 951.333 secs

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3	1001	100.0	15418	3	US-09-995-419A-1		Sequence 1, Appli
4	1001	100.0	15418	5	US-10-141-220-1		Sequence 1, Appli
5	1001	100.0	15418	5	US-10-023-969-1		Sequence 1, Appli
6	1001	100.0	15418	5	US-10-206-447-1		Sequence 1, Appli
7	1001	100.0	15418	7	US-10-674-836-1		Sequence 1, Appli
8	1001	100.0	15418	7	US-10-811-012-1		Sequence 1, Appli
9	988.4	98.7	5126	8	US-10-840-455-1		Sequence 3, Appli
10	988.4	98.7	11276	8	US-10-840-455-3		Sequence 3, Appli
11	988.4	98.7	26414	8	US-10-840-455-43		Sequence 43, Appl
12	988.4	98.7	51552	3	US-09-733-294A-30		Sequence 30, Appl
13	914.4	91.3	4293	8	US-10-456-830-1		Sequence 1, Appli
14	625.6	62.5	683	5	US-10-027-632-134480		Sequence 134480,
15	625.6	62.5	683	6	US-10-027-632-134480		Sequence 134480,
16	598	59.5	4356	7	US-10-240-589C-143		Sequence 143, App
17	535.8	53.5	4356	7	US-10-240-589C-144		Sequence 144, App
18	467.4	46.7	480	5	US-10-185-369-8		Sequence 8, Appli
19	60.2	6.0	610	4	US-09-925-065A-654088		Sequence 654088,
20	59.8	6.0	608	4	US-09-925-065A-663807		Sequence 663807,
21	56.6	5.7	622	4	US-09-925-065A-728894		Sequence 728894,
22	56.6	5.7	622	4	US-09-925-065A-728895		Sequence 728895,
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Db 9800 ATGCTCAAAAGAAAGAAATTTACCCATGACGAGGAGTGGTTGGGGGTTAAGGACGG 9859
Qy 361 TGGGGGACGACGCTGGGGGCTACTGACGCACTTTTAAAGCCAGTTTCTGGTTCT 420
Db 9860 TGGGGGACGACGCTGGGGGCTACTGACGCACTTTTAAAGCCAGTTTCTGGTTCT 9919
Qy 421 GATGGATTGGCTCAGTATGAGGAGTAAACCATAGGGGAGTGGGGAGGAAACCCGG 480
Db 9920 GATGGATTGGCTCAGTATGAGGAGTAAACCATAGGGGAGTGGGGAGGAAACCCGG 9979
Qy 481 AGGCTGGCCATCTTCCCATGCCCAGTGTCTCGGAGTGTCTTGGGAGGATAGCTTAGAGATGCC 540
Db 9980 AGGCTGGCCATCTTCCCATGCCCAGTGTCTCGGAGTGTCTTGGGAGGATAGCTTAGAGATGCC 10039
Qy 541 CACGCTCTGATTTCCCCCAAACTGTGACAGAAACCCCGCCGCGCCAGGGCCTTTGACGG 600
Db 10040 CACGCTCTGATTTCCCCCAAACTGTGACAGAAACCCCGCCGCGCCAGGGCCTTTGACGG 10099
Qy 601 TGTGATCTCCGTGAGGACCTGAGGTTGGGATCTTTCGGGACTACTGACGAGCCCGAAA 660
Db 10100 TGTGATCTCCGTGAGGACCTGAGGTTGGGATCTTTCGGGACTACTGACGAGCCCGAAA 10159
Qy 661 AGTAATCCAGGGTTCTGGGAAGAGCGGCGGAGGAGGTTGAGGGGGGAGGCTCAGGA 720
Db 10160 AGTAATCCAGGGTTCTGGGAAGAGCGGCGGAGGAGGTTGAGGGGGGAGGCTCAGGA 10219
Qy 721 CGATGAGGAGCAGTCACTGAGGCTGAAAGAGGAGGAGGAGGCTTCGAGCCAGGCTGCA 780
Db 10220 CGATGAGGAGCAGTCACTGAGGCTGAAAGAGGAGGAGGAGGCTTCGAGCCAGGCTGCA 10279
Qy 781 AGCGCTCCAGAGCTCGAAAAAGCGGGAGGAGACCTCCACGAGCCTGACAGAGGAA 840
Db 10280 AGCGCTCCAGAGCTCGAAAAAGCGGGAGGAGACCTCCACGAGCCTGACAGAGGAA 10339
Qy 841 GGCAAGCTGGCCCTTAGCCACGAGGCGCCATCGTGAGCTCGGCTCCGTCGCATAG 900
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Db 10400 GAGGGCACTCGCTGCTGCTTCTAGCATGAAGTGTGGGGATTTGCAAGCAACAGGA 10459
Qy 961 AACCCATGCACTGTGAATCTAGGATTTTCAAAACAAAGG 1001
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RESULT 2

US-09-994-427A-1
; Sequence 1, Application US/09994427A
; Patent No. US20020128221A1
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Schiff, J. Michael
; TITLE OF INVENTION: GLYCOSYLTRANSFERASE VECTORS FOR TREATING CANCER
; FILE REFERENCE: 083,002
; CURRENT APPLICATION NUMBER: US/09/994,427A
; CURRENT FILING DATE: 2002-02-26
; PRIOR FILING DATE: 2000-11-27
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 15418
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-994-427A-1

Query Match

100.0%; Score 1001; DB 3; Length 15418;

RESULT 3

Best Local Similarity 100.0%; Pred. No. 0;
Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 61 TAGCAGCATCATCTACACATCTCCGCTCCAGCAGCAGCCCGCTGTTTATTTTAAATAGC 120
Db 9560 TAGCAGCATCATCTACACATCTCCGCTCCAGCAGCAGCCCGCTGTTTATTTTAAATAGC 9619
Qy 121 TACAAGAGCAGGAAATTCCTGCTAAATATGCTTTTAAACAACTGGTTTAAACAAACGGGTC 180
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Qy 181 CATCCGACGCTGGAAGTTCCTCAAGTGAAGAGAAACATGCGTTTATAAAGCCCTGCA 240
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Qy 241 GGCATCTCAGGGAATTTACGCTGAGTCAAACTGCCACCTCCATGGGATAGTACGCAAC 300
Db 9740 GGCATCTCAGGGAATTTACGCTGAGTCAAACTGCCACCTCCATGGGATAGTACGCAAC 9799
Qy 301 ATGCTCAAAAGAAAGAAATTTACCCCATGCGAGGAGTGGTTGGGGGTTAAGGACGG 360
Db 9800 ATGCTCAAAAGAAAGAAATTTACCCCATGCGAGGAGTGGTTGGGGGTTAAGGACGG 9859
Qy 361 TGGGGGACGACGCTGGGGGCTACTGACGCACTTTTAAAGCCAGTTTCTGGTTCT 420
Db 9860 TGGGGGACGACGCTGGGGGCTACTGACGCACTTTTAAAGCCAGTTTCTGGTTCT 9919
Qy 421 GATGGATTGGCTCAGTATGAGGAGTAAACCATAGGGGAGTGGGGAGGAAACCCGG 480
Db 9920 GATGGATTGGCTCAGTATGAGGAGTAAACCATAGGGGAGTGGGGAGGAAACCCGG 9979
Qy 481 AGGCTGTGCCATCTTTCGATGCTGCTGCGGAGTGTCTTGGGAGGATAGCTTAGAGATGCC 540
Db 9980 AGGCTGTGCCATCTTTCGATGCTGCTGCGGAGTGTCTTGGGAGGATAGCTTAGAGATGCC 10039
Qy 541 CACGCTCTGATTTCCCCCAAACTGTGGAAGAGACCCCGCCGCGCCAGGGCCTTTGACGG 600
Db 10040 CACGCTCTGATTTCCCCCAAACTGTGGAAGAGACCCCGCCGCGCCAGGGCCTTTGACGG 10099
Qy 601 TGTGATCTCCGTGAGGACCTGAGGTTGGGATCTTTCGGGACTACTGACGAGCCCGAAA 660
Db 10100 TGTGATCTCCGTGAGGACCTGAGGTTGGGATCTTTCGGGACTACTGACGAGCCCGAAA 10159
Qy 661 AGTAATCCAGGGTTCTGGGAAGAGCGGCGGAGGAGGTTGAGGGGGGAGGCTCAGGA 720
Db 10160 AGTAATCCAGGGTTCTGGGAAGAGCGGCGGAGGAGGTTGAGGGGGGAGGCTCAGGA 10219
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Db 10220 CGATGAGGAGCAGTCACTGAGGCTGAAAGAGGAGGAGGAGGCTTCGAGCCAGGCTGCA 10279
Qy 781 AGCGCTCCAGAGCTCGAAAAAGCGGGAGGAGACCTCCACGAGCCTGACAGAGGAA 840
Db 10280 AGCGCTCCAGAGCTCGAAAAAGCGGGAGGAGACCTCCACGAGCCTGACAGAGGAA 10339
Qy 841 GGCAAGCTGGCCCTTAGCCACGAGGCGCCATCGTGAGCTCGGCTCCGTCGCATAG 900
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Qy 901 GAGGGCACTCGGCTGCTGCTTCTAGCATGAAGTGTGGGGATTTGCAAGCAACAGGA 960
Db 10400 GAGGGCACTCGGCTGCTGCTTCTAGCATGAAGTGTGGGGATTTGCAAGCAACAGGA 10459
Qy 961 GAGGGCACTCGGCTGCTGCTTCTAGCATGAAGTGTGGGGATTTGCAAGCAACAGGA 960
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 3: geneseqn2000s.*
- 4: geneseqn2001as.*
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- 10: geneseqn2003cs.*
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- 12: geneseqn2004as.*
- 13: geneseqn2004bs.*
- 14: geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1001	100.0	15418	6	Aa138601 Human TER
3	1001	100.0	15418	6	Ab54997 Lambda cl
4	1001	100.0	15418	6	Aa138595 DNA of pl
5	1001	100.0	15418	10	Adc21253 Lambda cl
6	988.4	98.7	5126	6	Aax88272 Human cat
7	988.4	98.7	51552	6	Aas96607 DNA encod
8	940.4	93.9	4356	13	Adu82633 Human hTE
9	914.4	91.3	4293	14	Adv23865 Human hTE
10	869.4	86.9	3962	4	Aa41091 Telomeras
11	598	59.7	4356	6	Ab192334 Chemical
12	535.8	53.5	4356	6	Ab192335 Chemical
13	467.4	46.7	480	8	Ab275670 Human TER
14	371	37.1	5491	13	Adu82631 Human hTE
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16	55	5.5	33737	6	Aa150815 Human can
17	50.2	5.0	223556	11	Acn44110 Human gen
18	50.2	5.0	243428	12	Adf51132 Human P-R
19	49.8	5.0	10732	3	Aa10594 Gene enco

c	20	48.8	4.9	430	5	ABA13896	Abal3896 Human ner
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c	22	48.6	4.9	1425	5	ABA20632	Abal20632 Human ner
c	23	48	4.8	2000	8	ADA71938	Ada71938 Rice gene
c	24	47.6	4.8	257645	12	ADQ97289	Adq97289 Human can
c	25	46.8	4.7	51719	6	AAD31365	Aad31365 52Kb gene
c	26	46.8	4.7	92139	6	AAD31364	Aad31364 92Kb gene
c	27	46.8	4.7	130320	10	ADF11613	Adf11613 Human scl
c	28	46.2	4.6	191010	12	ADO25291	Ado25291 Human pro
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c	32	44.8	4.5	12555	4	AAK78331	Aak78331 Human imm
c	33	44.8	4.5	12555	9	ADB60456	Adb60456 Connectiv
c	34	44.2	4.4	699	4	AAH92146	Aah92146 Human inf
c	35	43.6	4.4	108316	10	ADC87336	Adc87336 Human GPC
c	36	42.8	4.3	7967	14	ADX44917	Adx44917 Human gal
c	37	42.8	4.3	9821	14	ADX44918	Adx44918 Human gal
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c	39	42.8	4.3	96256	13	ADR53001	Adr53001 Drug ther
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ALIGNMENTS

RESULT 1

AAA63785

ID AAA63785 standard; DNA; 15418 BP.

AC AAA63785;

DT 04-DEC-2000 (first entry)

XX Nucleotide sequence of the human TERT promoter and gene from pGRN142.
XX Telomerase reverse transcriptase; TERT; promoter; telomerase complex;
XX telomere length; hyperplastic disease; cancer; oncolytic virus;
XX cis-acting transcriptional control sequence; viral replication;
XX cell proliferation; aging; immunological disorder; infertility; ss.

OS Homo sapiens.

PN WO200046355-A2.

PD 10-AUG-2000.

PF 04-FEB-2000; 2000WO-US003104.

PP 04-FEB-1999; 99US-00244438.

PR (GERO-) GERON CORP.

PI Morin GB, Lichtsteiner S, Vasserot A, Adams R, Cardozo LM;

PI Lebkowski JS;

PI WPI; 2000-532898/48.

XX New polynucleotides comprising cis-acting transcriptional control
XX sequences, e.g. promoter sequence, of telomerase reverse transcriptase
XX genes, useful in the treatment of cancer.

PS Claim 9; Page 58-61; 63pp; English.

XX The present sequence represents the human telomerase reverse
XX transcriptase (TERT) promoter and gene. TERT is part of the telomerase
XX complex responsible for maintaining telomere length and increasing
XX replicative capacity of progenitor cells. Telomerase activity is turned

off in mature differentiated cells, but is turned back on again in hyperplastic diseases, including many cancers. The polynucleotide comprises cis-acting transcriptional control sequences, e.g. promoter sequences in which a toxin or genetic element essential for viral replication is placed under the control of a TERT promoter. As a result, the virus replicates preferentially in cells expressing TERT, and selectively lyses cancer cells. The oncolytic viruses are useful for treating cancer in humans or animals. The TERT promoter sequences are useful in the treatment of cancer and other diseases of cell proliferation such as degenerative and aging processes and diseases of aging, immunological disorders, or infertility

SQ Sequence 15418 BP; 4518 A; 3797 C; 3765 G; 3338 T; 0 U; 0 Other;

Query Match 100.0%; Score 1001; DB 3; Length 15418;
Best Local Similarity 100.0%; Pred. No. 2.9e-289;
Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAAGACCCAGCATTTGGCACCCTCGACATTTGCCCCACAGCCCTGGGAATTCACGTGAC 60
DB 9500 AAAAGACCCAGCATTTGGCACCCTCGACATTTGCCCCACAGCCCTGGGAATTCACGTGAC 9559

QY 61 TAGCGCATCATGATACACATCCCGTCCACGACCGACCCCGCTGTTTATTTATATAGC 120
DB 9560 TAGCGCATCATGATACACATCCCGTCCACGACCGACCCCGCTGTTTATTTATATAGC 9619

QY 121 TACAAGCAGGAAATCCCTGCTAAATGTCCTTTAACAACCTGGTTAAACAACCGGTC 180
DB 9620 TACAAGCAGGAAATCCCTGCTAAATGTCCTTTAACAACCTGGTTAAACAACCGGTC 9679

QY 181 CATCCGACCGGTGACAGTTCCTCACAGTCAAGAGAAACATGCGCTTTATAAGCCCTGCA 240
DB 9680 CATCCGACCGGTGACAGTTCCTCACAGTCAAGAGAAACATGCGCTTTATAAGCCCTGCA 9739

QY 241 GGCATCTCAAGGGAATTTACGCTGAGTCAGTCAAACTGCCACCTCCATGGGATACGTACGCAAC 300
DB 9740 GGCATCTCAAGGGAATTTACGCTGAGTCAGTCAAACTGCCACCTCCATGGGATACGTACGCAAC 9799

QY 301 ATGCTCAAAAAGAAAGAAATTTCAACCCATCGCAGGAGGTGGTTGGGGGTTAAGACGG 360
DB 9800 ATGCTCAAAAAGAAAGAAATTTCAACCCATCGCAGGAGGTGGTTGGGGGTTAAGACGG 9859

QY 361 TGGGGCAGCAGCTGGGGGCTACGCACGACCTTTTACTAAGCCAGTTTCCTGCTTCT 420
DB 9860 TGGGGCAGCAGCTGGGGGCTACGCACGACCTTTTACTAAGCCAGTTTCCTGCTTCT 9919

QY 421 GATGTTATTCGCTCAGTTATGGGAGACTAACCATAGGGGAGTGGGATGGGGAAACCCGG 480
DB 9920 GATGTTATTCGCTCAGTTATGGGAGACTAACCATAGGGGAGTGGGATGGGGAAACCCGG 9979

QY 481 AGGCTGTGCCATCTTTGCCATGCCGAGTGTCTTGGGACGATAATGCTCTAGAGATGCC 540
DB 9980 AGGCTGTGCCATCTTTGCCATGCCGAGTGTCTTGGGACGATAATGCTCTAGAGATGCC 10039

QY 541 CAGTCTCTGATTTCCCAACCTGTGCAGACACCCCGCCCGCCCGCCCTTTCAGG 600
DB 10040 CAGTCTCTGATTTCCCAACCTGTGCAGACACCCCGCCCGCCCGCCCTTTCAGG 10099

QY 601 TGTGATCTCCGTGAGGACCTTGAGTCTGGGATCTTTCGGGACTACTCTGACGGCCCGGAAA 660
DB 10100 TGTGATCTCCGTGAGGACCTTGAGTCTGGGATCTTTCGGGACTACTCTGACGGCCCGGAAA 10159

QY 661 AGTAATCCAGGGTTCCTGGGAAGAGCGCGGACAGAGGGTCAGAGGGGGCGAGCTCAGGA 720
DB 10160 AGTAATCCAGGGTTCCTGGGAAGAGCGCGGACAGAGGGTCAGAGGGGGCGAGCTCAGGA 10219

QY 721 CGATGAGGCGAGTCAGTCTCAGGCTGAAGAGGAGGAGGGCTCCGAGCCAGGCTGCA 780
DB 10220 CGATGAGGCGAGTCAGTCTCAGGCTGAAGAGGAGGAGGGCTCCGAGCCAGGCTGCA 10279

QY 781 AGCGCTCTCCAGAAAGCTGGAATAAAGCGGGGAAGGACCCCTCCAGGAGCCCTGCAGCAGGAA 840

DB 10280 AGCGCTCTCAGAGACTGGAAAAAGCGGGAAGGACCCCTCCACGAGCCCTGCAGCAGGAA 10339

QY 841 GGCACGGCTGGCCCTTAGCCACCAGGGGCCCATCGTGGACCTCCGGCCTCCGTCGCATAG 900

DB 10340 GGCACGGCTGGCCCTTAGCCACCAGGGGCCCATCGTGGACCTCCGGCCTCCGTCGCATAG 10399

QY 901 GAGGGCACTCGCGCTCCCTTCTAGCATGAAGTGTGTGGGATTTGCAGAAGCAACACGGA 960

DB 10400 GAGGGCACTCGCGCTCCCTTCTAGCATGAAGTGTGTGGGATTTGCAGAAGCAACACGGA 10459

QY 961 AACCCATGCACCTGTAATCTAGGATTTATTTCAAACAAGG 1001

DB 10460 AACCCATGCACCTGTAATCTAGGATTTATTTCAAACAAGG 10500

RESULT 2
AAL38601
ID AAL38601 standard; DNA; 15418 BP.
XX
AC AAL38601;
XX
DT 16-AUG-2002 (first entry)
XX
Human TERT promoter and upstream sequence.
XX
DE Cytostatic; glycosyltransferase; tumour; cell-surface carbohydrate;
XX KW tissue specific; transcriptional control element; cancer cell;
XX KW gene therapy; human TERT; telomerase reverse transcriptase; ds.
XX OS Homo sapiens.
XX PN WO200242468-A2.
XX PD 30-MAY-2002.
XX 26-NOV-2001; 2001WO-US044306.
XX 27-NOV-2000; 2000US-0253395P.
XX (GERO-) GERON CORP.
XX Schiiff MJ;
XX WPI; 2002-479954/51.
XX
XX New polynucleotide encoding glycosyltransferase enzymes including histo
PT blood group transferase useful for treating conditions associated with
PT hyperproliferation, such as cancers and other neoplasias.
XX
PS Claim 9; Page 17-20; 49pp; English.

CC The invention relates to a polynucleotide comprising an encoding sequence
CC for a glycosyltransferase, under control of a heterologous tumour
CC specific or tissue specific transcriptional control element, where
CC expression of the polynucleotide in a human cell causes the cell to
CC express a cell-surface carbohydrate determinant to which some or all
CC humans have a naturally occurring antibody. The polynucleotide of the
CC invention is useful for killing cancer cells and for preparing a
CC medication for the treatment of cancer. The polynucleotide sequence of
CC the invention can be used to treat disorders by gene therapy. This
CC polynucleotide sequence represents the human TERT (telomerase reverse
CC transcriptase) promoter and upstream sequence related to the invention
XX
SQ Sequence 15418 BP; 4518 A; 3797 C; 3765 G; 3338 T; 0 U; 0 Other;

Query Match 100.0%; Score 1001; DB 6; Length 15418;
Best Local Similarity 100.0%; Pred. No. 2.9e-289;
Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAAGACCCAGCATTTGGCACCCTCGACATTTGCCCCACAGCCCTGGGAATTCACGTGAC 60

DB 9500 AAAAGACCCAGCATTTGGCACCCTCGACATTTGCCCCACAGCCCTGGGAATTCACGTGAC 9559

Db	9500	AAAAAAAAAGCCAGCAATTTGGCACCCCTTGGACATTTTGGCCCCACAGCCCTTGGGAATTCACGTGAC	9559
Qy	61	TACGCACATCATGTACACATCTCCCGTCTCAGCAGCCGACCCCGCTGTTTTATTATTAATAGC	120
Db	9560	TACGCACATCATGTACACATCTCCCGTCCAGCAGCCGACCCCGCTGTTTTATTATTAATAGC	9619
Qy	121	TACAAAGCAGGGAATCCCTGCTAAATGCTTTTAACAAACCTGGTTAAACAAACGGGTC	180
Db	9620	TACAAAGCAGGGAATCCCTGCTAAATGCTTTTAACAAACCTGGTTAAACAAACGGGTC	9679
Qy	181	CATCCGACAGCTGGACAGTTCTCTACAGTGAAGAGGAACAATGCCGTTTATAAAGCCTGCA	240
Db	9680	CATCCGACAGCTGGACAGTTCTCTACAGTGAAGAGGAACAATGCCGTTTATAAAGCCTGCA	9739
Qy	241	GGCATCTCAAGGGAATTACGCTGAGTCAAAACTGCGCACTCATGGGATACGTACGCAAC	300
Db	9740	GGCATCTCAAGGGAATTACGCTGAGTCAAAACTGCGCACTCATGGGATACGTACGCAAC	9799
Qy	301	ATGCTCAAAAGAAAGAAATTTTCAACCCCATGGCAGGGAGTGCTGGGGGTTTAAGGACGG	360
Db	9800	ATGCTCAAAAGAAAGAAATTTTCAACCCCATGGCAGGGAGTGCTGGGGGTTTAAGGACGG	9859
Qy	361	TGGGGGCAGCAGCTGGGGGCTACTGCAACGACCTTTTACTAAAGCAGTTTCTCGCTTCT	420
Db	9860	TGGGGGCAGCAGCTGGGGGCTACTGCAACGACCTTTTACTAAAGCAGTTTCTCGCTTCT	9919
Qy	421	GATGGTATTGGCTCAGTTATGGGAGACTAAACCATAGGGAGTGGGGATGGGGGAACCCGG	480
Db	9920	GATGGTATTGGCTCAGTTATGGGAGACTAAACCATAGGGAGTGGGGATGGGGGAACCCGG	9979
Qy	481	AGGCTGTGCCATCTTTTGCCATGCCCAGTGTCTCTGGGCAGGATAATGCTTAGAGATGCC	540
Db	9980	AGGCTGTGCCATCTTTTGCCATGCCCAGTGTCTCTGGGCAGGATAATGCTTAGAGATGCC	10039
Qy	541	CAGCTCTGATNTCCCCAAACCTGTGGACAGAACCCGCCCGGCCCCAGGGCTTTGCAAG	600
Db	10040	CAGCTCTGATNTCCCCAAACCTGTGGACAGAACCCGCCCGGCCCCAGGGCTTTGCAAG	10099
Qy	601	TGTGATCTCCGTCAGGACCTGAGTCTCGGATCTCTTCGGGACTACTGTGAGGCCCGGAAA	660
Db	10100	TGTGATCTCCGTCAGGACCTGAGTCTCGGATCTCTTCGGGACTACTGTGAGGCCCGGAAA	10159
Qy	661	AGTAATCCAGGGTTCTTGGGAAGAGCGGCGCAGGAGGTTCAGAGGGGGCAGCCTCAGGA	720
Db	10160	AGTAATCCAGGGTTCTTGGGAAGAGCGGCGCAGGAGGTTCAGAGGGGGCAGCCTCAGGA	10219
Qy	721	CGATGGAGCAGTCAGTCTGAGGCTGAAGAAGGAGGAGGGGCTCGAGCCCGAGGCTGCA	780
Db	10220	CGATGGAGCAGTCAGTCTGAGGCTGAAGAAGGAGGAGGGGCTCGAGCCCGAGGCTGCA	10279
Qy	781	AGGCCCTCCAGAAAGCTGGAAGAAGCGGGGAAGGGACCTTCCACGGAGCTCGCAGCAGGAA	840
Db	10280	AGGCCCTCCAGAAAGCTGGAAGAAGCGGGGAAGGGACCTTCCACGGAGCTCGCAGCAGGAA	10339
Qy	841	GGCAGGCTGGCCCTTAGCCACACAGGGCCCATCGTGTGACCTTCGGGCTTCGGTGCATAG	900
Db	10340	GGCAGGCTGGCCCTTAGCCACACAGGGCCCATCGTGTGACCTTCGGGCTTCGGTGCATAG	10399
Qy	901	GAGGGCACTCGCGCTGCCCTTCTAGCATGAAGTGTGTGGGATTTTGCAGAGCAACAGGA	960
Db	10400	GAGGGCACTCGCGCTGCCCTTCTAGCATGAAGTGTGTGGGATTTTGCAGAGCAACAGGA	10459
Qy	961	AACCCATGCACTGTGAATCTTAGGATTTATTCAAAAAAGG	1001
Db	10460	AACCCATGCACTGTGAATCTTAGGATTTATTCAAAAAAGG	10500

RESULT 4
AAL38595
ID AAL
XX
AC AAL

XX	16-AUG-2002 (first entry)
DT	
XX	DNA of plasmid pGRN144 containing human hTERT gene.
DE	
XX	
XX	Anticonvulsant; cerebroprotective; vasotropic; neurotropic; stem cell;
KW	neuroprotective; antiparkinsonian; antiinflammatory; undifferentiated;
KW	cardiant; transcriptional control element; human embryonic; tissue graft;
KW	regenerative medicine; tissue reconstruction; neural progenitor cell;
KW	nerve system; epilepsy; stroke; ischaemia; Huntington's disease;
KW	parkinson's disease; multiple sclerosis; leukodystrophy; neuritis;
KW	hepatocyte; liver damage; cardiomyocyte; cryoinjury; cardiac muscle;
KW	pGRN144; human hTERT gene; chimeric; ds.
XX	
OS	Homo sapiens.
OS	Unidentified.
OS	Chimeric.
XX	
XX	WO200242445-A2.
XX	
XX	30-MAY-2002.
FD	
XX	
XX	26-NOV-2001; 2001WO-US044309.
PF	
XX	
XX	27-NOV-2000; 2000US-0253357P.
FR	
FR	27-NOV-2000; 2000US-0253443P.
FR	13-FEB-2001; 2001US-00783203.
XX	
XX	(GERO-) GERON CORP.
PA	
XX	
PI	Gold JD, Lebrowski JS;
PI	
XX	WPI; 2002-479952/51.
DR	
XX	
XX	Depleting a cell e.g., human embryonic stem cell population of
PT	undifferentiated stem cells (UC) for use in regenerative medicine
PT	comprises genetically altering UC in a population to express nucleic acid
PT	encoding a lethal product.
XX	
FS	Example 9; Page 62-66; 67pp; English.
XX	
CC	The invention relates to a system for depleting a cell population of
CC	undifferentiated stem cells, by introducing nucleic acids of structure P-
CC	X, where X is a nucleic acid encoding product that is lethal to a cell in
CC	which it is expressed; or renders a cell in which it is expressed
CC	susceptible to the lethal effect of an external agent, and P is a
CC	transcriptional control element causing X to be preferentially expressed
CC	in the undifferentiated stem cells. The system is used for depleting a
CC	cell population (preferably, human embryonic stem cells) of
CC	undifferentiated stem cells. A population of differentiated cells is
CC	useful in regenerative medicine, and for preparing antibodies and cDNA
CC	libraries that are specific for a differentiated phenotype. The cell
CC	populations are also useful for drug screening and therapeutic
CC	applications. The differentiated cells are useful for tissue
CC	reconstitution or regeneration in a human patient in need of treatment.
CC	The cells are administered in a manner that permits to graft to the
CC	intended tissue side and reconstitute or regenerate the functionally
CC	deficient area. The neural progenitor cells are useful for treating acute
CC	or chronic damage to the nerve system e.g. epilepsy, stroke, ischaemia,
CC	Huntington's disease, Parkinson's disease, multiple sclerosis,
CC	leukodystrophies, neuritis, etc. The hepatocytes and hepatocyte
CC	precursors are useful for assessing animal models for ability to repair
CC	liver damage. The cardiomyocyte population is useful for assessing animal
CC	models for cryoinjury, regenerating cardiac muscle and to treat
CC	insufficient cardiac function. This polynucleotide sequence represents
CC	the DNA of plasmid pGRN144 containing the human hTERT gene relating to
CC	the invention

Query Match 100.0%; Score 1001; DB 6; Length 15418;
Best Local Similarity 100.0%; Pred. No. 2.9e-289;
Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAAGACCCAGCATTTGGCACCCTCGGACATTTGGCCACACAGCCCTGGGAATTCACGTGAC 60
DB 9500 AAAAGACCCAGCATTTGGCACCCTCGGACATTTGGCCACACAGCCCTGGGAATTCACGTGAC 9559
QY 61 TACGCACATCATGTACACATCTCCGTCACAGCCAGCCCGCTGTTTATTTAAATAGC 120
DB 9560 TACGCACATCATGTACACATCTCCGTCACAGCCAGCCCGCTGTTTATTTAAATAGC 9619
QY 121 TACAAGCAGGGAATCCCTGCTAAATGTCCTTTACAACTGTTTAAACAAACGGGTC 180
DB 9620 TACAAGCAGGGAATCCCTGCTAAATGTCCTTTAACTGTTTAAACAAACGGGTC 9679
QY 181 CATCCGACGGTGACAGTCTCTCACTGAGAGGACATGCCGTTTATAAAGCCGTGCA 240
DB 9680 CATCCGACGGTGACAGTCTCTCACTGAGAGGACATGCCGTTTATAAAGCCGTGCA 9739
QY 241 GGCATCTCAAGGGAATTAACGTGAGTCAAACTGCCACCTCCATGGGATAGTACGCAAC 300
DB 9740 GGCATCTCAAGGGAATTAACGTGAGTCAAACTGCCACCTCCATGGGATAGTACGCAAC 9799
QY 301 ATGCTCAAAAAGAAATTTACCCCATGCGAGGAGTGTGTTGGGGGTTAAGGACGG 360
DB 9800 ATGCTCAAAAAGAAATTTACCCCATGCGAGGAGTGTGTTGGGGGTTAAGGACGG 9859
QY 361 TGGGGGACGAGCTGGGGGCTACTGACGACACCTTTTACTAAAGCCAGTTTCTCTGGTTCT 420
DB 9860 TGGGGGACGAGCTGGGGGCTACTGACGACACCTTTTACTAAAGCCAGTTTCTCTGGTTCT 9919
QY 421 GATGGTATTTGGCTCAGTTATGGGAGACTAAACATAGGGGAGTGGGGGAAACCCGG 480
DB 9920 GATGGTATTTGGCTCAGTTATGGGAGACTAAACATAGGGGAGTGGGGGAAACCCGG 9979
QY 481 AGGCTGTGCCATCTTTGCGCATGCCGAGTGTCTGGGACAGGATATGCTCTAGAGATGCC 540
DB 9980 AGGCTGTGCCATCTTTGCGCATGCCGAGTGTCTGGGACAGGATATGCTCTAGAGATGCC 10039
QY 541 CAGCTCTGATTTCCCAAACTGTGGACAGAACCCCGCCGCGGCTTTGACGG 600
DB 10040 CAGCTCTGATTTCCCAAACTGTGGACAGAACCCCGCCGCGGCTTTGACGG 10099
QY 601 TGTGATCTCCGTGAGGACCTGAGTCTGGGATCTTCGGGACTACCTGACAGGCCCGAAA 660
DB 10100 TGTGATCTCCGTGAGGACCTGAGTCTGGGATCTTCGGGACTACCTGACAGGCCCGAAA 10159
QY 661 AGTAATCAGGGGTTCTGGGAAGAGCGCGGACGAGGTCAGAGGGGCGAGCTTCAGGA 720
DB 10160 AGTAATCAGGGGTTCTGGGAAGAGCGCGGACGAGGTCAGAGGGGCGAGCTTCAGGA 10219
QY 721 CGATGGAGCAGTCAGTCTGAGGCTGAAAGAGGAGGAGGCGCTCGAGCCAGGCTGCA 780
DB 10220 CGATGGAGCAGTCAGTCTGAGGCTGAAAGAGGAGGAGGCGCTCGAGCCAGGCTGCA 10279
QY 781 AGCGCTCCAGAGCTGAAAAGCGGGAAGGACCTTCCACGAGAGCTTCAGCAGGAA 840
DB 10280 AGCGCTCCAGAGCTGAAAAGCGGGAAGGACCTTCCACGAGAGCTTCAGCAGGAA 10339
QY 841 GGCACGGCTGCGCTTACCCACACAGGCGCCATCGTGGACCTCGCGCTCGCATAG 900
DB 10340 GGCACGGCTGCGCTTACCCACACAGGCGCCATCGTGGACCTCGCGCTCGCATAG 10399
QY 901 GAGGCACTCGGCTGCGCTTCTAGCATGAAGTGTGGGATTTGCAAGACGACAGGA 960
DB 10400 GAGGCACTCGGCTGCGCTTCTAGCATGAAGTGTGGGATTTGCAAGACGACAGGA 10459
QY 961 AACCCATGCACTGTAATCTAGGATTTTCAAAACAAAGG 1001
DB 10460 AACCCATGCACTGTAATCTAGGATTTTCAAAACAAAGG 10500

RESULT 5
ADC21253
ID ADC21253 standard; DNA; 15418 BP.

XX ADC21253;
AC 18-DEC-2003 (first entry)
DB Lambda clone (lambdaGph15) containing human TERT DNA.
XX Viral vector; heterologous control element; gene expression;
XX human telomerase reverse transcriptase; hTERT; tumour specific gene;
XX cell death; transcriptional control element;
XX human telomerase RNA component; hTR; cancer cell; liver cancer;
XX prostate cancer; muscle cancer; neural cell cancer; lung cancer;
XX pancreatic cancer; medulloblastoma; cervical carcinoma; fibrosarcoma;
XX osteosarcoma; lambda clone; lambdaGph15; human; ds.
OS Synthetic.
OS Homo sapiens.
OS Bacteriophage lambda.
XX US2003099616-A1.
XX 29-MAY-2003.
XX 25-JUL-2002; 2002US-00206447.
XX 25-JUL-2001; 2001US-0308029P.
XX (IRVI/) IRVING J M.
XX (KARP/) KARP D B.
XX (SCHI/) SCHIFF J M.
XX Irving JM, Karpf DB, Schiff JM;
XX WPI; 2003-730140/69.
XX New dual specificity vectors driven by the telomerase promoter, useful
XX for killing or slowing the growth of tumor cells, or for treating cancer,
XX e.g. liver cancer, prostate cancer, lung cancer, or pancreatic cancer.
XX Example 1; Page 13-20; 25pp; English.
XX The present invention relates to a viral vector comprising first and
XX second genes controlled by heterologous control elements, where the first
XX gene is preferentially expressed in cells expressing human telomerase
XX reverse transcriptase (hTERT), and another gene under the control of a
XX heterologous transcriptional control element for a tissue or tumour
XX specific gene other than TERT, and where transduction of the vector into
XX a mammalian cell expressing TERT causes the death of the cell or its
XX progeny. In particular, the second gene may be under the control of a
XX transcriptional control element for a tissue specific gene selected from
XX albumin, alpha-fetoprotein, prostate-specific antigen, mitochondrial
XX creatine kinase, myelin basic protein, glial fibrillary acidic protein,
XX and neuron-specific enolase. The second gene may be under the control of
XX a transcriptional control element for a human telomerase RNA component
XX (hTR). The vector of the invention is useful for killing a cancer cell,
XX or treating a subject for a condition associated with increased
XX expression of TERT in affected cells. The vector is also useful in the
XX preparation of a medicament for treatment of a condition associated with
XX increased expression of TERT, particularly cancer, and especially liver
XX cancer, prostate cancer, muscle cancer, neural cell cancer, lung cancer,
XX pancreatic cancer, medulloblastoma, cervical carcinoma, fibrosarcoma, and
XX osteosarcoma. The present sequence represents a lambda clone
XX (lambdaGph15) containing human TERT DNA.
SQ Sequence 15418 BP; 4518 A; 3797 C; 3765 G; 3338 T; 0 U; 0 Other;

Query Match 100.0%; Score 1001; DB 10; Length 15418;
Best Local Similarity 100.0%; Pred. No. 2.9e-289;
Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


```
Qy 480 GAGCTGTGCCATCTTTGCCATGCCCGAGTGTCTCTGGCGAGGATAATGCTCTAGAGATGC 539
Db 1559 GAGCTGTGCCATCTTTGCCATGCCCGAGTGTCTCTGGCGAGGATAATGCTCTAGAGATGC 1618
Qy 540 CCAGTCTCTGATTTCCCGAAACCTGTGTGAAGAACCCTGGCCCGCCAGGCGCTTTTGCGAG 599
Db 1619 CCAGTCTCTGATTTCCCGAAACCTGTGTGAAGAACCCTGGCCCGCCAGGCGCTTTTGCGAG 1678
Qy 600 GTGTGATCTCCGTGAGAGACCTGAGGTCTGGATCTCTGGGACTTACTGTCAGGCCCGAA 659
Db 1679 GTGTGATCTCCGTGAGAGACCTGAGGTCTGGATCTCTGGGACTTACTGTCAGGCCCGAA 1738
Qy 660 AAGTAATCCAGGGGTCTTGGGAAGAGCGGCGAGAGGGTTCAGAGGGGGGCGAGCTCAGG 719
Db 1739 AAGTAATCCAGGGGTCTTGGGAAGAGCGGCGAGAGGGTTCAGAGGGGGGCGAGCTCAGG 1798
Qy 720 ACATGAGGAGCAGTCAAGTCTGAGGCTGAAGAGGAGGAGGGCCCTCGAGGCCAGGCTGTC 779
Db 1799 ACATGAGGAGCAGTCAAGTCTGAGGCTGAAGAGGAGGAGGGCCCTCGAGGCCAGGCTGTC 1858
Qy 780 AAGCGCTCCAGAGAGCTGGAAGAGCGGGGAAGGAGCCCTCCAGCGAGCCTGCGAGCAGGA 839
Db 1859 AAGCGCTCCAGAGAGCTGGAAGAGCGGGGAAGGAGCCCTCCAGCGAGCCTGCGAGCAGGA 1918
Qy 840 AGGCAAGGCTGGCCCTTAGCCACACAGGGCCATCGTGAGCTCCGGCTCCGTGCCATA 899
Db 1919 AGGCAAGGCTGGCCCTTAGCCACACAGGGCCATCGTGAGCTCCGGCTCCGTGCCATA 1978
Qy 900 GGAGGGCACTCGCGTGCCTTCTAGCATGAAGTGTGTGGGATTTGCAAGCAACAGG 959
Db 1979 GGAGGGCACTCGCGTGCCTTCTAGCATGAAGTGTGTGGGATTTGCAAGCAACAGG 2038
Qy 960 AAACCCATGCACTGTGAATCTAGGATTTTCAAAACAAAGG 1001
Db 2039 AAACCCATGCACTGTGAATCTAGGATTTTCAAAACAAAGG 2080

RESULT 7
AAS96607
ID AAS96607 standard; DNA; 51552 BP.
AC AAS96607;
XX
XX
DT 09-APR-2002 (first entry)
XX
DE DNA encoding human telomerase reverse transcriptase (TERT) #1.
KW Telomerase reverse transcriptase; TERT; cytosolic; apoptosis;
KW cell growth inhibitor; antisense oligonucleotide; antisense technology;
KW ds.
XX
OS Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FT exon 1..11492
FT /tag= a
FT /number= 1
FT CDS 11274..47813
FT /tag= b
FT /product= "TERT"
FT /note= "Telomerase reverse transcriptase"
FT intron 11493..11596
FT /tag= c
FT /number= 1
FT exon 11597..12950
FT /tag= d
FT /number= 2
FT intron 12951..21566
FT /tag= e
FT /number= 2
FT exon 21567..21762
FT /tag= f
FT /number= 3
FT intron 21763..23851
FT /tag= g
FT /number= 3
FT exon 23852..24032
FT /tag= h
FT /number= 4
FT intron 24033..24719
FT /tag= i
FT /number= 4
FT exon 24720..24899
FT /tag= j
FT /number= 5
FT intron 24900..25393
FT /tag= k
FT /number= 5
FT exon 25394..25549
FT /tag= l
FT /number= 6
FT intron 25550..30195
FT /tag= m
FT /number= 6
FT exon 30196..30292
FT /tag= n
FT /number= 7
FT intron 30293..31272
FT /tag= o
FT /number= 7
FT exon 31273..31358
FT /tag= p
FT /number= 8
FT intron 31359..33843
FT /tag= q
FT /number= 8
FT exon 33844..33957
FT /tag= r
FT /number= 9
FT intron 33958..35941
FT /tag= s
FT /number= 9
FT exon 35942..36013
FT /tag= t
FT /number= 10
FT intron 36014..37884
FT /tag= u
FT /number= 10
FT exon 37885..38073
FT /tag= v
FT /number= 11
FT intron 38074..41874
FT /tag= w
FT /number= 11
FT exon 41875..42001
FT /tag= x
FT /number= 12
FT intron 42002..42881
FT /tag= y
FT /number= 12
FT exon 42882..42943
FT /tag= z
FT /number= 13
FT intron 42944..46129
FT /tag= aa
FT /number= 13
FT exon 46130..46254
FT /tag= ab
FT /number= 14
FT intron 46255..47035
FT /tag= ac
FT /number= 14
FT exon 47036..47173
FT /tag= ad
FT /number= 15
FT intron 47174..47709
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XX	WO2004099377-A2.	QY	48	GAATTCACGTGATACGCAATCATGTACACATCTCCGTCACACGACCCCGCTGTT	107
PN		DB	1	GAATTCACGTGATACGCAATCATGTACACATCTCCGTCACACGACCCCGCTGTT	60
XX	18-NOV-2004.	QY	108	TTATTTTAATAGCTACAAAGCGGGAATCCCTGCTAAATGTCCTTTAAACAATGTT	167
XX	30-APR-2004; 2004WO-US013487.	DB	61	TTATTTTAATAGCTACAAAGCGGGAATCCCTGCTAAATGTCCTTTAAACAATGTT	120
XX	01-MAY-2003; 2003US-0467171P.	QY	168	AAACAAACGGGTCCATCCGACCGGTGACAGATTCCTCACAGTGAAGAGGAACATGCGGTT	227
XX	(MUSC-) MUSC FOUND RES DEV.	DB	121	AAACAAACGGGTCCATCCGACCGGTGACAGATTCCTCACAGTGAAGAGGAACATGCGGTT	180
PI	Dong J, Rubinchik S, Woraratanadham J;	QY	228	TATAAAGCCTGCGAGGCAATCAAGGGAATACGCTGAGTCAAAATGCGACCTCATGCGG	287
XX	WPI; 2004-805118/79.	DB	181	TATAAAGCCTGCGAGGCAATCAAGGGAATACGCTGAGTCAAAATGCGACCTCATGCGG	240
DR	P-PSDB; ADU82634.	QY	288	ATAGCTACGCAACATGCTCAAAAGAAAGAAATTTTCAACCCATGCGAGGAGTGGTGGG	347
DR	GENBANK; AF097365.	DB	241	ATAGCTACGCAACATGCTCAAAAGAAAGAAATTTTCAACCCATGCGAGGAGTGGTGGG	299
XX	New expression vector comprising a first expression cassette with a first	QY	348	GGGTAAAGGACGGTGGGGGCGAGCAGCTGGGGGCTACTGCGACGACCTTTTAAAGCCA	407
XX	coding region that encodes a transcriptional activating factor (TAF),	DB	300	GGGTAAAGGACGGTGGGGGCGAGCAGCTGGGGGCTACTGCGACGACCTTTTAAAGCCA	359
XX	useful in treating cancer, AIDS, hemophilia, diabetes and asthma.	QY	408	GTTCCTCTGCTGATGATGCTTATGCTCAGTTATGGGAGACTAAACATAGGAGGAGTGGGA	467
PS	Disclosure; SEQ ID NO 5; 112pp; English.	DB	360	GTTCCTCTGCTGATGATGCTTATGCTCAGTTATGGGAGACTAAACATAGGAGGAGTGGGA	419
XX	The invention relates to an expression vector comprising a first	QY	468	TGGGGGAACCGGAGGCTGTCATCTTTCATGTCGCGGAGTGTCTTGGGAGGATATG	527
CC	expression cassette having a first coding region that encodes a	DB	420	TGGGGGAACCGGAGGCTGTCATCTTTCATGTCGCGGAGTGTCTTGGGAGGATATG	479
CC	transcriptional activating factor (TAF), and a second expression cassette	QY	528	CTCTAGAGATGCCACAGCTGCTGATTTCCCTCCCAAACTGTGGACAGAACCCGCGGCCCA	587
CC	comprising a second coding region that encodes a selected polypeptide.	DB	480	CTCTAGAGATGCCACAGCTGCTGATTTCCCTCCCAAACTGTGGACAGAACCCGCGGCCCA	539
CC	The expression vector further comprises a first expression cassette	QY	588	GGGCTTTTGCAGGTGTGATCTCTCGTGAGGACCTCTGAGTCTTGGGATCTTCTGGGACTACC	647
CC	having a first coding region that encodes a transcriptional activating	DB	540	GGGCTTTTGCAGGTGTGATCTCTCGTGAGGACCTCTGAGTCTTGGGATCTTCTGGGACTACC	599
CC	factor (TAF), the first coding region being positioned under the	QY	648	TGCAGGCCGGAAGATTAATCCAGGGGTTCTGGGAAGAGCGCGGAGGAGGCTCAGAGGGG	707
CC	transcriptional control of a first promoter comprising a tissue specific	DB	600	TGCAGGCCGGAAGATTAATCCAGGGGTTCTGGGAAGAGCGCGGAGGAGGCTCAGAGGGG	659
CC	regulatory element (TSRE), and a TAF binding site (TBS), and a second	QY	708	GCCAGCCTCAGACGATGAGGCGAGTCACTCTGAGGCTGAAAAGGAGGAGGAGGCTCGA	767
CC	expression cassette comprising a second coding region that encodes a	DB	660	GCCAGCCTCAGACGATGAGGCGAGTCACTCTGAGGCTGAAAAGGAGGAGGAGGCTCGA	719
CC	selected polypeptide, the second coding region being positioned under the	QY	768	GCCAGCCTCAGACGATGAGGCGAGTCACTCTGAGGCTGAAAAGGAGGAGGAGGCTCGA	827
CC	transcriptional control of a second promoter comprising a TSRE and a TBS,	DB	720	GCCAGCCTCAGACGATGAGGCGAGTCACTCTGAGGCTGAAAAGGAGGAGGAGGCTCGA	779
CC	or a TBS. The expression vector further comprises a third coding region	QY	828	CCTGAGCAGGAAGGACGCGCTGCGCTTACCCACAGGCGGCCATCTGACACTCCGCG	887
CC	that encodes a first transcriptional silencer (TSI), the third coding	DB	780	CCTGAGCAGGAAGGACGCGCTGCGCTTACCCACAGGCGGCCATCTGACACTCCGCG	839
CC	region being positioned under the transcriptional control, a third	QY	888	CTCCGTCCTATAGGAGGCACTCCGCTGCGCTTCTAGCATGAGTGTGGGATTTGCG	947
CC	promoter comprising a TSRE and a TBS, and a fourth expression cassette	DB	840	CTCCGTCCTATAGGAGGCACTCCGCTGCGCTTCTAGCATGAGTGTGGGATTTGCG	899
CC	comprising a fourth coding region that encodes a second TSI, the fourth	QY	948	AGAAAGCAACAGGAACCCATGCACTGTGAATCTAGGATTTTCAAAACAAGG 1001	
CC	coding region being positioned under the transcriptional control of a	DB	900	AGAAAGCAACAGGAACCCATGCACTGTGAATCTAGGATTTTCAAAACAAGG 953	
CC	fourth promoter that is negatively regulated by the first TSI, where the	XX	ADV23865	ADV23865	
CC	first, second and third promoters are negatively regulated by the second	XX	ADV23865	ADV23865	
CC	TSI. The selected polypeptide is a therapeutic polypeptide, such as an	XX	24-FEB-2005	(first entry)	
CC	anti-cancer polypeptide that is a tumor suppressor, and inducer of	XX			
CC	apoptosis, and cell cycle regulator, a toxin, or an inhibitor of				
CC	angiogenesis, and an enzyme, a cytokine, a hormone, a tumor antigen, a				
CC	human antigen or a pathogen antigen. The selected polypeptide is				
CC	essential for vector replication, where the vector is an adenoviral				
CC	vector. The expression vector is useful in methods for treating cancer				
CC	and further comprises a selectable or screenable marker. The methods and				
CC	compositions of the present invention are useful in the fields of				
CC	molecular biology and gene therapy, particularly to the combined spatial				
CC	and quantitative regulation of transgene expression in eukaryotic cells,				
CC	and in treating cancer including breast cancer, ovarian cancer, fallopian				
CC	tube cancer, cervical cancer, uterine cancer, prostate cancer, testicular				
CC	cancer, pancreatic cancer, colon cancer, bladder cancer, liver cancer,				
CC	stomach cancer, lung cancer, lymphoid cancer, brain cancer, thyroid				
CC	cancer, head and neck cancer, skin cancer or leukemia. The cancer is a				
CC	recurrent cancer, a metastatic cancer or a drug resistant cancer. The				
CC	methods and compositions can also be used in treating cystic fibrosis,				
CC	AIDS, sickle cell anemia, hemophilia, diabetes, heart disease, asthma				
CC	inflammatory disorders, rheumatoid arthritis, multiple sclerosis, and				
CC	reverse transcriptase (HTRT) gene nucleotide sequence, the promoter				
CC	fragment can be used in the vectors of the invention.				
XX	Sequence 4356 BP; 829 A; 1298 C; 1254 G; 975 T; 0 U; 0 Other;				
XX	Query Match 93.9%; Score 940.4; DB 13; Length 4356;				
XX	Best Local Similarity 99.8%; Pred. No. 2.7e-271;				
XX	Matches 952; Conservative 0; Mismatches 1; Indels 1; Gaps 1;				

QY 314 AAGAAATTTACCCATGCGAGGGAGTGGTTGGGGGTTAAGACAGCGTGGGGGAGCAGC 373
DB 241 AAGATTTTACCCATGCGAGGGAGTGGTT-GGGGGTTAAGACAGCGTGGGGGAGCAGC 299
QY 374 TGGGGGCTACTGCGACGACACCTTTTACTAAAGCCAGTTTCTGGTTCTGATGGTATGGCT 433
DB 300 TGGGGGCTACTGCGACGACACCTTTTACTAAAGCCAGTTTCTGGTTCTGATGGTATGGCT 359
QY 434 CAGTTATGGAGACTAACCATAGGGGAGTGGGGATGGGGAGCCCGAGGCTGTGCCATC 493
DB 360 CAGTTATGGAGACTAACCATAGGGGAGTGGGGATGGGGAGCCCGAGGCTGTGCCATC 419
QY 494 TTTGCCATGCCCGAGTGTCTGGGCGAGGATAATCTCTAGAGATGCCACGCTCTGATTC 553
DB 420 TTTGCCATGCCCGAGTGTCTGGGCGAGGATAATCTCTAGAGATGCCACGCTCTGATTC 479
QY 554 CCCCAGAACCTGTGTGACAGAAACCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCC 613
DB 480 CCCCAGAACCTGTGTGACAGAAACCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCC 539
QY 614 AGGACCTTGAGGTCTGGATCTCTGGGACTACCTGCGAGCCCGGAGGAGTAAATCCAGGG 673
DB 540 AGGACCTTGAGGTCTGGATCTCTGGGACTACCTGCGAGCCCGGAGGAGTAAATCCAGGG 599
QY 674 TTCTGGGAAGAGCGCGGCGAGGAGGTCTAGAGGGGGGAGCCCTCAGGACGATGGAGGAGT 733
DB 600 TTCTGGGAAGAGCGCGGCGAGGAGGTCTAGAGGGGGGAGCCCTCAGGACGATGGAGGAGT 659
QY 734 CAGTCTGAGGCTGAAAAGGGAGGGAGGCGCTTCGAGCCCGAGCCCTGCAAGCGCCCTCCAGAA 793
DB 660 CAGTCTGAGGCTGAAAAGGGAGGGAGGCGCTTCGAGCCCGAGCCCTGCAAGCGCCCTCCAGAA 719
QY 794 GCTGGAAAAAGCGGGGAAGGAGACCTTCAGCGAGCTGCGAGGAGGAGGAGGAGGAGGAGG 853
DB 720 GCTGGAAAAAGCGGGGAAGGAGACCTTCAGCGAGCTGCGAGGAGGAGGAGGAGGAGGAGG 779
QY 854 CTTAGCCCAACAGGCGCCATCGTGAGCTTCGGGCTTCGGGCTTCGGGCTTCGGGCTTCGGG 913
DB 780 CTTAGCCCAACAGGCGCCATCGTGAGCTTCGGGCTTCGGGCTTCGGGCTTCGGGCTTCGGG 839
QY 914 CTGCGCTTCTAGCATGAAGTGTGGGGATTTGAGAGCAACAGGAAACCCATGCACTG 973
DB 840 CTGCGCTTCTAGCATGAAGTGTGGGGATTTGAGAGCAACAGGAAACCCATGCACTG 899
QY 974 TGAATCTAGGATTAATTTCAAAACAAAG 1001
DB 900 TGAATCTAGGATTAATTTCAAAACAAAG 927

RESULT 10
AAH41091
ID AAH41091 standard; DNA; 3962 BP.

AC AAH41091;

DT 29-AUG-2001 (first entry)

DE Telomerase reverse transcriptase (TERT) DNA.

KW Phenotype switch molecule; phenotype-related gene battery;
KW gene localisation; telomere reverse transcriptase; TERT; ds.

OS Unidentified.

PN WO200138515-A1.

XX 31-MAY-2001.

XX 17-NOV-2000; 2000WO-CN000427.

XX 19-NOV-1999; 99CN-00121466.

(BIAN/) BIAN X.

PI Bian X;

XX WPI; 2001-367684/38.

DR XX Isolating phenotype switch molecules and phenotype-related gene batteries
PT from complex genomes of higher animals and plants, useful e.g. in gene
PT localization and classification analysis.

XX Example 7; Page 27-29; 35pp; Chinese.

PS This invention relates to a method for isolating phenotype switch
XX molecules and phenotype-related gene batteries from complex genomes of
CC higher animals and plants. The method is useful in gene localisation and
CC classification analysis, studying gene development networks and function
CC networks, and designing drugs based on regulatory sequences of the
CC phenotypes for disease treatment. The present sequence represents DNA
CC encoding a telomere reverse transcriptase (TERT), which is used in an
CC example illustrating the use of the method of the invention

XX Sequence 3962 BP; 782 A; 1157 C; 1113 G; 910 T; 0 U; 0 Other;

Query Match 86.9%; Score 869.4; DB 4; Length 3962;

Best Local Similarity 99.8%; Pred. No. 5.5e-250;

Matches 881; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 119 GCTACAAGCAGGGGAATCCCTGCTAAATGTCTTTAAACAACCTGGTTAAACAACCGG 178
DB 1 GCTACAAGCAGGGGAATCCCTGCTAAATGTCTTTAAACAACCTGGTTAAACAACCGG 60
QY 179 TCCATCCGCGAGGTCGACAGTTCTCAGTGAAGAGGAACATCCGCTTTATAAGCCTG 238
DB 61 TCCATCCGCGAGGTCGACAGTTCTCAGTGAAGAGGAACATCCGCTTTATAAGCCTG 120
QY 239 CAGGCATCTCAGGGAAATAGCTGAGTCAAAACTGCCACCTCATGGGATACGTACGCA 298
DB 121 CAGGCATCTCAGGGAAATAGCTGAGTCAAAACTGCCACCTCATGGGATACGTACGCA 180
QY 299 ACATGCTCAAAAAGAAAGATTTTCAACCCATGGCAGGGAGTGGTTGGGGGTTAAGGAC 358
DB 181 ACATGCTCAAAAAGAAAGATTTTCAACCCATGGCAGGGAGTGGTT-GGGGGTTAAGGAC 239
QY 359 GGTGGGGGAGCAGCTGGGGGCTACTGCACACCTTTTACTAAAGCAGTTTCTGTGTT 418
DB 240 GGTGGGGGAGCAGCTGGGGGCTACTGCACACCTTTTACTAAAGCAGTTTCTGTGTT 299
QY 419 CTGATGGTATTGGCTCAGTTATGGGAGACTAACCATAGGGGAGTGGGATGGGGAAACCC 478
DB 300 CTGATGGTATTGGCTCAGTTATGGGAGACTAACCATAGGGGAGTGGGATGGGGAAACCC 359
QY 479 GGAGGCTGTGCATCTTTGCCATGCCGAGTGTCTTGGGAGGATTAATGCTTAGAGATG 538
DB 360 GGAGGCTGTGCATCTTTGCCATGCCGAGTGTCTTGGGAGGATTAATGCTTAGAGATG 419
QY 539 CCCAGCTCTGATTCCTCCCAACCTGTGGACAGAACCCCGCCCGCCCGCCCGCCCGCCCG 598
DB 420 CCCAGCTCTGATTCCTCCCAACCTGTGGACAGAACCCCGCCCGCCCGCCCGCCCGCCCG 479
QY 599 GGTGTGATCTCCGTGAGGACCTTGAAGTCTGGGATCTTTCGGGACTACTGCGAGCCCGA 658
DB 480 GGTGTGATCTCCGTGAGGACCTTGAAGTCTGGGATCTTTCGGGACTACTGCGAGCCCGA 539
QY 659 AAAGTAATCCAGGGGTTCTGGGAAGAGCGGGCAGGAGGTTTCAAGGGGGGCGAGCTCAG 718
DB 540 AAAGTAATCCAGGGGTTCTGGGAAGAGCGGGCAGGAGGTTTCAAGGGGGGCGAGCTCAG 599
QY 719 GACGATGAGGAGCTCAGTCTGAGGCTGAAAAGGAGGAGGAGGCTTCGAGCCCGAGCCTG 778
DB 600 GACGATGAGGAGCTCAGTCTGAGGCTGAAAAGGAGGAGGAGGCTTCGAGCCCGAGCCTG 659
QY 779 CAAGCGCTCCAGGAAGCTTGGAAAAGCGGGGAAGGAGCCCTCCACGAGGCTTCGACGAGG 838

RESULT 12	Db	4295	TATTTTAACTACAAAAAATAAATCCCTACTAAAAATATCTTTTAAACAAATAATTA	4236
ABL92335/c	Qy	169	AACAAACGGGTCCATCCGACGGTGGACAGTTCCTCACAGTGAAGAGAGAAACATCCCGTTT	228
ID ABL92335 standard; DNA; 4356 BP.	Db	4235	AACAAACGAATCCATCCGACGATAAACAATTCCTCAATATAAAAAAACAATACCGTTT	4176
XX ABL92335;	Qy	229	ATAAAGCCTCAGGCATCTCAAGGGAAATTACGTGAGTCAAAACTGCCACCTCCATGGGA	288
01-JUL-2002 (first entry)	Db	4175	ATRAAACCTACAAACATCTCAAAAAAATAAGCTAAATCAAACTACCACTCCATAAAA	4116
Chemically treated DNA repair gene fragment complementary to #72.	Qy	289	TACGTAGCAACATGCTCAAAAAGAAAGATTTTACCCCATGGCAGGGAGTGTGGGG	348
DNA repair; cytosine methylation; PMS2L1; PMS2L2; PMS2L3; PMS2;	Db	4115	TACGTAGCAACATGCTCAAAAAGAAAGATTTTACCCCATGGCAGGGAGTGTGGGG	4057
L4; PMS2L5; PMS2L6; MGMT; MSH2; NUDT1; TDG; INPPL1; RFC4; DDITL1; FANCB;	Qy	349	GTTTAAAGCAGGTGGGGGACGAGCTGCGGGCTACTGCAGCACCTTTTACTAAAGCCAG	408
XRC8; ataxia telangiectasia; aging; Bloom's syndrome; Cockayne syndrome;	Db	4056	AAITAAAAACGATAAAAACCAACTAAATACTACTACGACCTTTTCTATAAACCA	3997
Nijmegen breakage syndrome; Werner syndrome; immunodeficiency;	Qy	409	TTTCTGTTCTGATGTTTGGCTCAGTTATGGGAGACTAAACATAGGGAGTGGGAT	468
trichiodystrophy; Fanconi's anaemia; solid tumour; cancer; ds.	Db	3996	TTTCTGTTCTGATGTTTGGCTCAGTTATGGGAGACTAAACATAGGGAGTGGGAT	3937
Unidentified.	Qy	469	GGGGAAACCCGGAGCTGTGCTTTTGCATGCGCGAGTGTCTTGGGAGGATAATGC	528
WO200181622-A2.	Db	3936	AAAAAAACCCGAAACATATACCATCTTTACCATACCCGAAATATCTTAAACAAAATAATAC	3877
01-NOV-2001.	Qy	529	TCTAGATGCGCCACGCTCTGATTTCCGCCAACCTGTGGACAGACCGCCGCGCCAG	588
06-APR-2001; 2001WO-EP003972.	Db	3876	TCTAAAAATACCCACGCTCTTAAATTTCCCCCAAACTATATAACAAACCCGCGCCCA	3817
06-APR-2000; 2000DE-01019058.	Qy	589	GGCCTTTGCGAGTGTGATCTCCGAGAGACCTCAGGTCTGGGATCTTCCGGGACTACT	648
07-APR-2000; 2000DE-01019173.	Db	3816	AACCTTTTCAATATATATCTCCGTAAAAACCTTAAATCTTAAATCTTCAAACTACT	3757
30-JUN-2000; 2000DE-01032529.	Qy	649	GCAGGCCCGAAAAAGTAAATCCAGGGGTTCTGGGAAAGAGCGGGAGGGGTCAGAGGGG	708
01-SEP-2000; 2000DE-01043826.	Db	3756	ACAAACCCGAAAAATAATCCAAAAATTTCTAAAAAAGAGCGAAACAAAAAATAA	3697
(EPIG-) EPIGENOMICS AG.	Qy	709	GCAGCCTCAGGACGATGGAGGCGCTCAGTCTGAGGCTGAAAGGGAGGGGCGCTCGAG	768
Olek A, Piepenbrock C, Berlin K;	Db	3696	ACAACTCAAAACGATAAAAACCAATCAATCTTAAACCTAAAAAATAAATAAATAA	3637
WPI; 2002-034446/04.	Qy	769	CCAGGCGCTCAGAGCGCTCCAGAGCTGGAAGAGCGGGAGGAGCCCTCCACGGAGC	828
New nucleic acid derived from genes associated with DNA repair, useful	Db	3636	CCCAAACTCAAAACGCTCCAAAACTTAAAAAATAAATAAATAAATAAATAAATAA	3577
for diagnosis, e.g. of ataxia telangiectasia, by determination of	Qy	829	CTGACGAGGAGGACGCGCTGGCCCTTAGCCACACGAGGGCCCATCGTGGACCTCCG	888
cytosine methylation.	Db	3576	CTACAAACAAAAAACACGACTAAACCTTAAACCCCAAAACCCATCGTAAACCTCCG	3517
Claim 1; SEQ ID NO 144; 25pp + Sequence Listing; English.	Qy	889	TCCGTGCTATAGGAGGCGCTCCGCGCTTCTAGCATGAAGTGTGCGGATTTGCA	948
The invention relates to nucleic acids containing a sequence of at least	Db	3516	TCCGTGCTATAGGAGGCGCTCCGCGCTTCTAGCATGAAGTGTGCGGATTTGCA	3457
18 nucleotides of chemically treated DNA of genes associated with DNA	Qy	949	GAACCAACAGAAACCCATGCATCTGCAATCTAGGATTTTCAAAACAAA	999
repair, and their complements. The invention also relates to nucleic	Db	3456	AAAAACAAACAAAAACCCATACACTATATTAATTAATTTTCAAAACAAA	3406
acids comprising at least 18 base pairs of the chemically pretreated DNA	RESULT 13			
of genes associated with DNA repair selected from PMS2L1, PMS2L2,	ABL9235670	ID	AB275670 standard; DNA; 480 BP.	
PMS2L3, PMS2L4, PMS2L5, PMS2L6, MGMT, MSH2, NUDT1, TDG, INPPL1,	XX	XX	AB275670;	
RFC4, DDITL1, FANCB, or XRC8. Nucleic acids of the invention and related	XX	XX	15-MAY-2003 (first entry)	
oligonucleotides are useful for diagnosis of diseases associated with gene	XX	XX	Human TERT promoter region.	
repair, specifically ataxia telangiectasia, aging, Bloom's syndrome,	XX	XX	HLTF; carcinogenesis; hyperproliferative lesion; cytostatic; virucide;	
Cockayne syndrome, Nijmegen breakage syndrome or Werner syndrome,	XX	XX	helicase-like transcription factor; telomerase reverse transcriptase;	
immunodeficiency, trichiodystrophy, Fanconi's anaemia, solid tumours	XX	XX	dermatological; gynaecological; TERT; gene therapy; cancer; ds.	
and cancer, particularly by determining status of cytosine methylation				
and/or by detecting single-nucleotide polymorphisms. Determination of				
individual methylation patterns may allow development of individualised				
therapies. The sequences given in records ABL92192-ABL92335 represent				
chemically pre-treated DNA fragments from genes associated with DNA				
repair, and their complements. Note: The sequence data for this patent is				
not represented in the specification, but is based on sequence				
information supplied by the European Patent Office				
Sequence 4356 BP; 975 A; 218 C; 1298 G; 1865 T; 0 U; 0 Other;				
Query Match 53.5%; Score 535.8; DB 6; Length 4356;				
Best Local Similarity 73.4%; Pred. No. 9.9e-150;				
Matches 698; Conservative 0; Mismatches 253; Indels 1; Gaps 1;				
Qy 49 AATTCACGTGATAGGACATCATGTACACACTCCGTCACGACCGACCCCGCTGTTT				108
Db 4355 AATTCACGTGATAGGACATCATGTACACACTCCGTCACGACCGACCCCGCTGTTT				4296
Qy 109 TATTTTAACTACAAAAAATAAATCCCTACTAAAAATATCTTTTAAACAAATAATTA				168


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XX OS Homo sapiens.
XX PN WO2003002068-A2.
XX PD 09-JAN-2003.
XX PF 27-JUN-2002; 2002WO-US020757.
XX PR 27-JUN-2001; 2001US-0301384P.
XX PA (NEWB-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.
XX PI Androphy EJ, Doshi N, Delayew A;
XX PF WI; 2003-210197/20.
XX PT Inhibiting carcinogenesis of a cell, especially useful for treating a
XX PT human papilloma virus-mediated hyperproliferative lesion (warts) or
XX PT cancer, by reducing the activity of helicase-like transcription factor in
XX PT the cell.
XX PS Claim 18; Fig 6; 36pp; English.
XX CC The invention relates to inhibiting carcinogenesis of a cell, or
XX CC inhibiting growth of a cell in a human papillomavirus (HPV)-mediated
XX CC hyperproliferative lesion. The method involves reducing the amount of
XX CC helicase-like transcription factor (HLTF) in the cell or inhibiting the
XX CC binding of endogenous HLTF to telomerase reverse transcriptase (TERT)
XX CC promoter. The method is useful for inhibiting carcinogenesis of a cell,
XX CC or inhibiting growth of a cell in an HPV-mediated hyperproliferative
XX CC lesion. The method is particularly useful for treating cancer (especially
XX CC cervical cancer), or hyperproliferative lesions (warts) caused by HPV.
XX CC The method is also useful for diagnosing a neoplasm, or detecting the
XX CC presence of a malignant tumour or a predisposition to developing the
XX CC tumour. The present sequence represents the hTERT promoter region to
XX CC which HLTF binds to
XX SQ Sequence 480 BP; 125 A; 117 C; 131 G; 107 T; 0 U; 0 Other;

Query Match 46.7%; Score 467.4; DB 8; Length 480;
Best Local Similarity 99.6%; Pred. No. 1.3e-129;
Matches 479; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 48 GAATTCACGCTACGACATCATGTACACATCCCGTCCAGCAGCGACCCCGCTGTT 107
DB 1 GAATTCACGCTACGACATCATGTACACATCCCGTCCAGCAGCGACCCCGCTGTT 60

QY 108 TTATTTTAATAGCTACAAAGCAGGGAATCCCTGCTAAAATGCTTTAAACAACTGGTT 167
DB 61 TTATTTTAATAGCTACAAAGCAGGGAATCCCTGCTAAAATGCTTTAAACAACTGGTT 120

QY 168 AAACAAACGGGTCCATCCGACCGGTGGACAGTTCCTCAGAGTGAAGAGGAACATGCCGTT 227
DB 121 AAACAAACGGGTCCATCCGACCGGTGGACAGTTCCTCAGAGTGAAGAGGAACATGCCGTT 180

QY 228 TATAAGCCTGCAGGATCTCAAGGGAATTCAGCTAGTCAAACTCCACCTCCATGGG 287
DB 181 TATAAGCCTGCAGGATCTCAAGGGAATTCAGCTAGTCAAACTCCACCTCCATGGG 240

QY 288 ATAGTACGCAACATGCTCAAAAGAAAGAAATTTACCCCATGCGAGGAGTGTGGG 347
DB 241 ATAGTACGCAACATGCTCAAAAGAAAGAAATTTACCCCATGCGAGGAGTGTGGT-GG 299

QY 348 GGGTTAAGGACGGTGGGGGAGCAGCTGGGGGCTACTGCAAGCACTTTTACTAAAGCCA 407
DB 300 GGGTTAAGGACGGTGGGGGAGCAGCTGGGGGCTACTGCAAGCACTTTTACTAAAGCCA 359

QY 408 GTTTCCTGGTCTGATGGTATGCTCAGTTATGGGAGACTAACCATAGGGAGTGGGA 467
DB 360 GTTTCCTGGTCTGATGGTATGCTCAGTTATGGGAGACTAACCATAGGGAGTGGGA 419

QY 468 TGGGGGAACCGGAGGCTGTGCCATCTTTGCCATGCCGAGTGTCTCTGGGCGAGGATAATG 527
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Db 420 TGGGGGACCCGGAGGCTGTGCCATCTTTGCCATGCCGAGTCTCTGGGCGAGGATAATG 479
QY 528 C 528
DB 480 C 480

RESULT 14
ADU82631
ID ADU82631 standard; DNA; 5491 BP.
XX AC ADU82631;
XX DT 10-FEB-2005 (first entry)
XX DE Human hTERT gene nucleotide sequence.
XX KW Gene expression; transcription; TERT; telomerase reverse transcriptase;
XX KW cancer therapy; cytostatic; CNS; respiratory; anti-HIV; anti-anemic;
XX KW antischlicking; hemostatic; antidiabetic; cardiant; antiinflammatory;
XX KW antirheumatic; antiarthritic; neuroprotective; antiasthmatic; vasotropic;
XX KW gene therapy; apoptosis stimulator; cancer; gene; ds.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT CDS 3415..3633
XX FT /tag= a
XX FT /product= "telomerase reverse transcriptase fragment"
XX FT /partial
XX PN WO200409377-A2.
XX XX 18-NOV-2004.
XX XX 30-APR-2004; 2004WO-US013487.
XX XX 01-MAY-2003; 2003US-0467171P.
XX XX (MUSC-) MUSC FOUND RES DEV.
XX XX Dong J, Rubinchik S, Woraratanadham J;
XX XX WPI; 2004-805118/79.
XX XX P-PSDB; ADU82632.
XX XX GENBANK; AB016767.
XX XX New expression vector comprising a first expression cassette with a first
XX XX coding region that encodes a transcriptional activating factor (TAF),
XX XX useful in treating cancer, AIDS, hemophilia, diabetes and asthma.
XX PS Disclosure; SEQ ID NO 3; 112pp; English.
XX XX The invention relates to an expression vector comprising a first
XX XX expression cassette having a first coding region that encodes a
XX XX transcriptional activating factor (TAF), and a second expression cassette
XX XX comprising a second coding region that encodes a selected polypeptide.
XX XX The expression vector further comprises a first expression cassette
XX XX having a first coding region that encodes a transcriptional activating
XX XX factor (TAF), the first coding region being positioned under the
XX XX transcriptional control of a first promoter comprising a tissue specific
XX XX regulatory element (TSRE), and a TAF binding site (TBS), and a second
XX XX expression cassette comprising a second coding region that encodes a
XX XX selected polypeptide, the second coding region being positioned under the
XX XX transcriptional control of a second promoter comprising a TSRE and a TBS,
XX XX or a TBS. The expression vector further comprises a third coding region
XX XX that encodes a first transcriptional silencer (TSI), the third coding
XX XX region being positioned under the transcriptional control, a third
XX XX promoter comprising a TSRE and a TAF, and a fourth expression cassette
XX XX comprising a fourth coding region that encodes a second TSI, the fourth
XX XX coding region being positioned under the transcriptional control of a
XX XX fourth promoter that is negatively regulated by the first TSI, where the
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CC first, second and third promoters are negatively regulated by the second
CC TSI. The selected polypeptide is a therapeutic polypeptide, such as an
CC anti-cancer polypeptide that is a tumor suppressor, and inducer of
CC apoptosis, and cell cycle regulator, a toxin, or an inhibitor of
CC angiogenesis, and an enzyme, a cytokine, a hormone, a tumor antigen, a
CC human antigen or a pathogen antigen. The selected polypeptide is
CC essential for vector replication, where the vector is an adenoviral
CC vector. The expression vector is useful in methods for treating cancer
CC and further comprises a selectable or screenable marker. The methods and
CC compositions of the present invention are useful in the fields of
CC molecular biology and gene therapy, particularly to the combined spatial
CC and quantitative regulation of transgene expression in eukaryotic cells,
CC and in treating cancer including breast cancer, ovarian cancer, fallopian
CC tube cancer, cervical cancer, uterine cancer, prostate cancer, testicular
CC cancer, pancreatic cancer, colon cancer, bladder cancer, liver cancer,
CC stomach cancer, lung cancer, lymphoid cancer, brain cancer, thyroid
CC cancer, head and neck cancer, skin cancer or leukemia. The cancer is a
CC recurrent cancer, a metastatic cancer or a drug resistant cancer. The
CC methods and compositions can also be used in treating cystic fibrosis,
CC AIDS, sickle cell anemia, hemophilia, diabetes, heart disease,
CC inflammatory disorders, rheumatoid arthritis, multiple sclerosis, asthma
CC and restenosis. The present invention represents a human telomerase
CC reverse transcriptase (hTERT) gene nucleotide sequence, the promoter
CC fragment can be used in the vectors of the invention.

SQ Sequence 5491 BP; 954 A; 1729 C; 1677 G; 1131 T; 0 U; 0 Other;

Query Match 37.1%; Score 371; DB 13; Length 5491;
Best Local Similarity 100.0%; Pred. No. 3.6e-100;
Matches 371; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 631 GATCCTTCGGGACCTACCTGACGGCCGCGAAAGTAAATCCAGGGGTTCTGGGAGAGGCGGG 690
DB 1 GATCCTTCGGGACCTACCTGACGGCCGCGAAAGTAAATCCAGGGGTTCTGGGAGAGGCGGG 60
QY 691 CAGGAGGGTTCAGAGGGGGGCGACCTCAGGACGATGGAGGCGAGTCAGTCTGAGGCTGAAAA 750
DB 61 CAGGAGGGTTCAGAGGGGGGCGACCTCAGGACGATGGAGGCGAGTCAGTCTGAGGCTGAAAA 120
QY 751 GGGAGGAGGGGCTTCGAGCCCGAGGCTGCAAGCGCTTCAGAGCTGGAAGAGGCGGGA 810
DB 121 GGGAGGAGGGGCTTCGAGCCCGAGGCTGCAAGCGCTTCAGAGCTGGAAGAGGCGGGA 180
QY 811 AGGACCTTCACGGAGGCTCAGCAGAGGAGGCGGCTGCGCTTACGCCACAGGGCC 870
DB 181 AGGACCTTCACGGAGGCTCAGCAGAGGAGGCGGCTGCGCTTACGCCACAGGGCC 240
QY 871 CATCGTGACCTCGGGCTCCGTCATAGAGGCGCACTCGCGTGCCTTCTAGCATGA 930
DB 241 CATCGTGACCTCGGGCTCCGTCATAGAGGCGCACTCGCGTGCCTTCTAGCATGA 300
QY 931 AGTGTGTGGGATTTCAGAGAGCAACAGGAACCCATGCACTGTGAATCTAGGATTTT 990
DB 301 AGTGTGTGGGATTTCAGAGAGCAACAGGAACCCATGCACTGTGAATCTAGGATTTT 360
QY 991 CAACAACAAGG 1001
DB 361 CAACAACAAGG 371

RESULT 15
AAA41829
ID AAA41829 standard; cDNA; 467 BP.
XX
XX
XX AAA41829;
XX
XX
XX 21-AUG-2000 (first entry)
XX Human secreted expressed sequence tag SEQ ID NO:569.
DE
DE Human; mouse; xenopus; rat; secreted expressed sequence tag; sEST;
XX expressed sequence tag; EST; probe; chemotactic; proliferative;
XX immunomodulatory; haematopoietic; chemokinetic; analgesic; haemostatic;

thrombolytic; antiinflammatory; cytostatic; antibacterial; antifungal;
KW antiviral; antidiabetic; antiasthmatic; vulnary; antiparkinsonian;
KW antitumor; osteopathic; neuroprotective; nootropic; antiparkinsonian;
KW cerebroprotective; anticonvulsant; antidepressant; gene therapy; vaccine;
KW autoimmune disorder; multiple sclerosis; allergic condition;
KW insulin dependent diabetes; asthma; myeloid cell deficiency; ulcer;
KW lymphoid cell deficiency; burn; osteoporosis; osteoarthritis;
KW central nervous system disorder; Alzheimer's disease; stroke;
KW Parkinson's disease; Huntington's disease; coagulation disorder;
KW haemophilia; thrombosis; inflammatory disorder; Crohn's disease; tumour;
KW infection; depression; psoriasis; ss.

Homo sapiens.

WO200021990-A1.

20-APR-2000.

15-OCT-1999; 99WO-US024205.

15-OCT-1998; 98US-0104435P.

(GBMY) GENETICS INST INC.

Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C;

Merberg D, Treacy M;

WPI; 2000-317937/27.

Isolated polynucleotides, and encoded proteins, comprising secreted
expressed sequence tags (sESTs), useful for treating various disorders
such as autoimmune, infectious, and central nervous system disorders.

Claim 1; Page 290; 618pp; English.

AAA41261 to AAA43419 represent specifically claimed secreted expressed
sequence tags (sESTs), isolated from human, mouse, xenopus and rat tissue
sources. The sESTs can have a range of activities depending on the
tissues they were isolated from. The activities include: chemotactic;
proliferative; immunomodulatory; haematopoietic; chemokinetic; analgesic;
haemostatic; thrombolytic; antiinflammatory; cytostatic; antibacterial;
antifungal; antiviral; antidiabetic; antiasthmatic; vulnary; antitumor;
osteopathic; neuroprotective; nootropic; antiparkinsonian; antipsoriatic;
cerebroprotective; anticonvulsant; and antidepressant. The sESTs can be
used for gene therapy and in vaccines. The sESTs are useful as probes for
the identification and isolation of full-length cDNAs and genomic DNA
molecules which correspond to the sESTs. Proteins encoded by the sESTs
are useful in assays for determining biological activity and raising
antibodies. They may be useful for treatment of autoimmune disorders
(multiple sclerosis, insulin dependent diabetes), allergic conditions
(asthma), myeloid or lymphoid cell deficiencies, wounds, burns, ulcers,
osteoporosis, osteoarthritis, central nervous system disorders
(Alzheimer's, Parkinson's, Huntington's disease, stroke), coagulation
disorders (haemophilia, thrombosis), inflammatory disorders (Crohn's
disease), tumours, bacterial, fungal or viral infections, depression and
psoriasis. AAA43420 to AAA43425 represent linker variants which are given
in the exemplification of the present invention

Sequence 467 BP; 134 A; 96 C; 134 G; 103 T; 0 U; 0 Other;

Query Match 5.8%; Score 57.6; DB 3; Length 467;
Best Local Similarity 61.7%; Pred. No. 1.7e-06;
Matches 142; Conservative 0; Mismatches 84; Indels 4; Gaps 3;
QY 587 AGGGCCTTTGACGGTGTGATCTCCGTGAGGACCTCGAGGTCTGG-GATCCTTCGGGACTA 645
DB 221 AGGGACITTCAGGGGTGACTGAGTAAAGGATCCTCAGATGAGGAGGTTTTCATGGATTG 280
QY 646 CCTGAGGCCCGAAAAAGTAATCCAGGGGTTCTGGGAGAGGCGGCGAGGCTCAGAGG 705
DB 281 TTTGGTGGGCCCCAATGTAATCCAGGATCCTTTCAAGCAAGGAGGCGGCGAGG 340
QY 706 GGGGCGGCT--CAGGACGATGGAGGCGAGTCAGTCTGAGGCTGAAAGGAGGAGGCGCC 763

Db	341	CAGAGAAACAGACACGACAAATGGAAGCAGAGGTTGGGTTGATACTGGAGTGGGAGGGGCC	400
Qy	764	TCGAGCCCGCCCTGCAGC-GCCTCCAGAGCTTGGNAAAAGCGGGGAAG	812
Db	401	ACGAGCCAGGAATGCAGGCAGCCTTAGGAGCTTGGNAAAAGGCAAGAAAG	450

Search completed: January 10, 2006, 11:12:03
Job time : 694.667 secs

Dowell, R.
091615039
Seq. 101

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 10, 2006, 10:08:59 ; Search time 5387 Seconds
(without alignments)
10562.520 Million cell updates/sec

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Perfect score: 1001
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb in.*
3: gb env.*
4: gb om.*
5: gb ov.*
6: gb pat.*
7: gb ph.*
8: gb pr.*
9: gb ro.*
10: gb sts.*
11: gb sy.*
12: gb un.*
13: gb vi.*
14: gb btg.*
15: gb pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1001	100.0	15332	8 AF121948	AF121948 Homo sapi
2	1001	100.0	15418	6 AR342806	AR342806 Sequence
3	1001	100.0	15418	6 AR490112	AR490112 Sequence
4	1001	100.0	15418	6 AR576878	AR576878 Sequence
5	1001	100.0	15418	6 AX453025	AX453025 Sequence
6	1001	100.0	15418	6 AX498409	AX498409 Sequence
7	1001	100.0	15418	6 AX504952	AX504952 Sequence
8	1001	100.0	92564	8 AY007685	AY007685 Homo sapi
9	1001	100.0	161252	14 AC114955	AC114955 Homo sapi
10	988.4	98.7	5126	6 AX003120	AX003120 Sequence
11	988.4	98.7	11276	6 AX003122	AX003122 Sequence
12	988.4	98.7	12213	8 AF114847	AF114847 Homo sapi
13	988.4	98.7	26414	8 HSTRT1	AF128893 Homo sapi
14	988.4	98.7	51552	6 AR266023	AR266023 Sequence
15	988.4	98.7	202305	8 AC114291	AC114291 Homo sapi
16	946	94.5	170646	14 AC123545	AC123545 Pan trogl
17	940.4	93.9	4356	8 AF097365	AF097365 Homo sapi
18	744.4	74.4	170946	14 AC117933	AC117933 Papio anu

c 19	744.4	74.4	183506	14	AC122155	AC122155 Papio anu
c 20	598	59.7	4356	6	AX356509	AX356509 Sequence
c 21	535.8	53.5	4356	6	AX356510	AX356510 Sequence
c 22	371	37.1	5491	8	AB016767	AB016767 Homo sapi
c 23	62.8	6.3	250175	14	AC160494	AC160494 Bos tauru
c 24	61.2	6.1	149252	8	AC012615	AC012615 Homo sapi
c 25	60.2	6.0	175225	14	AC136941	AC136941 Homo sapi
c 26	60.2	6.0	185228	8	CNS01RGU	AL160192 Human chr
c 27	58.8	5.9	627	10	BV436875	BV436875 S237P6476
c 28	58.8	5.9	187395	14	AC164243	AC164243 Bos tauru
c 29	58.8	5.9	260185	14	AC160299	AC160299 Bos tauru
c 30	57.6	5.8	44495	8	AL589846	AL589846 Human DNA
c 31	56.6	5.7	166287	8	AC002060	AC002060 Homo sapi
c 32	56.6	5.7	171995	14	AC149702	AC149702 Bos tauru
c 33	56.2	5.6	178630	14	AC016219	AC016219 Homo sapi
c 34	56.2	5.6	181914	8	AC009154	AC009154 Homo sapi
c 35	55.8	5.6	74625	8	AL596214	AL596214 Human DNA
c 36	55.8	5.6	161691	14	AC021385	AC021385 Homo sapi
c 37	55.6	5.6	142638	8	AL355316	AL355316 Human DNA
c 38	55.4	5.5	156899	14	AC103884	AC103884 Homo sapi
c 39	55.4	5.5	176797	8	AC116552	AC116552 Homo sapi
c 40	55.4	5.5	190590	14	AC135045	AC135045 Homo sapi
c 41	55	5.5	33737	6	BD176844	BD176844 A method
c 42	55	5.5	33737	8	HSIGLAMB	XS1755 Human lamod
c 43	55	5.5	40162	8	D87017	D87017 Homo sapien
c 44	55	5.5	125020	8	AF429315	AF429315 Homo sapi
c 45	54.4	5.4	169104	8	AL162377	AL162377 Human DNA

ALIGNMENTS

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LOCUS	AF121948	AF121948	15332 bp	DNA	reverse transcriptase (TERT) gene, partial cds.	
DEFINITION	AF121948	AF121948	15332 bp	DNA	reverse transcriptase (TERT) gene, partial cds.	
ACCESSION	AF121948	AF121948	1	GI:4580662		
VERSION	AF121948	AF121948	1	GI:4580662		
KEYWORDS	AF121948	AF121948	1	GI:4580662		
SOURCE	AF121948	AF121948	1	GI:4580662		
ORGANISM	AF121948	AF121948	1	GI:4580662		
REFERENCE	AF121948	AF121948	1	GI:4580662		
AUTHORS	AF121948	AF121948	1	GI:4580662		
TITLE	AF121948	AF121948	1	GI:4580662		
JOURNAL	AF121948	AF121948	1	GI:4580662		
PUBMED	AF121948	AF121948	1	GI:4580662		
REFERENCE	AF121948	AF121948	1	GI:4580662		
AUTHORS	AF121948	AF121948	1	GI:4580662		
TITLE	AF121948	AF121948	1	GI:4580662		
JOURNAL	AF121948	AF121948	1	GI:4580662		
FEATURES	AF121948	AF121948	1	GI:4580662		
source	AF121948	AF121948	1	GI:4580662		
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mRNA	AF121948	AF121948	1	GI:4580662		
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RPAEATLSEGLASGTRHSHPSVQRQHHAGFPSTSRPPRPWDPTPCPVVATKHFPLYS
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ORIGIN

Query Match 100.0%; Score 1001; DB 8; Length 15332;
Best Local Similarity 100.0%; Pred. No. 9.1e-272;
Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAAGACCCAGCATTTGGCACCCCTGGACATTTGCCACAGCCCTCGGAAATTCACGCTGAC 60
Db 9457 AAAAGACCCAGCATTTGGCACCCCTGGACATTTGCCACAGCCCTCGGAAATTCACGCTGAC 9516

Qy 61 TAGCGACATCATGTACACACTCCCGTCCAGCAGCCGACCCCGCTGTTTTTATTTTAAATAGC 120
Db 9517 TAGCGACATCATGTACACACTCCCGTCCAGCAGCCGACCCCGCTGTTTTTATTTTAAATAGC 9576

Qy 121 TACAAGCAGGGAATCCCTGCTAAATGTCCTTTTAAACAACTGGTTTAAACAAACGGGTC 180
Db 9577 TACAAGCAGGGAATCCCTGCTAAATGTCCTTTTAAACAACTGGTTTAAACAAACGGGTC 9636

Qy 181 CATCCGACCGGTGCACAGTTCTCCACAGTGAAGAGGAACATCGCTTTTATAAAGCCCTGCA 240
Db 9637 CATCCGACCGGTGCACAGTTCTCCACAGTGAAGAGGAACATCGCTTTTATAAAGCCCTGCA 9696

Qy 241 GGCATCTCAAGGGAATTAACGTGAGTCAAACTGCCACCTCCATGGGATAGTACGACGAC 300
Db 9697 GGCATCTCAAGGGAATTAACGTGAGTCAAACTGCCACCTCCATGGGATAGTACGACGAC 9756

Qy 301 ATGCTCAAAAAGAAAGAAATTTACCCCATCGCAGGAGAGTGGTTGGGGGGTTAAGGACGG 360
Db 9757 ATGCTCAAAAAGAAAGAAATTTACCCCATCGCAGGAGAGTGGTTGGGGGGTTAAGGACGG 9816

Qy 361 TGGGGGACAGCTGGGGGCTACTGCACGACCTTTTACTTAAAGCCAGTTTCTCGTTCT 420
Db 9817 TGGGGGACAGCTGGGGGCTACTGCACGACCTTTTACTTAAAGCCAGTTTCTCGTTCT 9876

Qy 421 GATGGTATTGGCTCAGTTATGGGAGACTAAACATAGGGGAGTGGGATGGGGAAACCCGG 480
Db 9877 GATGGTATTGGCTCAGTTATGGGAGACTAAACATAGGGGAGTGGGATGGGGAAACCCGG 9936

Qy 481 AGGCTGTGCCATCTTTGCCATGCCCAGAGTGTCTTGGGACGAGTAATGCTCTAGAGATGCC 540
Db 9937 AGGCTGTGCCATCTTTGCCATGCCCAGAGTGTCTTGGGACGAGTAATGCTCTAGAGATGCC 9996

Qy 541 CAGCTCTGTATCCCCCAACCTGTGACAGAACCCCGCCCGCCAGGGCCCTTTCAGG 600
Db 9997 CAGCTCTGTATCCCCCAACCTGTGACAGAACCCCGCCCGCCAGGGCCCTTTCAGG 10056

Qy 601 TGTGATCTCCGTAGGACCTCGAGTCTGGGATCTCTTGGGACTTACCTGACGGCCCGAAA 660
Db 10057 TGTGATCTCCGTAGGACCTCGAGTCTGGGATCTCTTGGGACTTACCTGACGGCCCGAAA 10116

Qy 661 AGTAATCCAGGGGTTCTGGGAAGAGCGGGCAGGAGGTCAGAGGGGGCAGGCTCTCAGGA 720
Db 10117 AGTAATCCAGGGGTTCTGGGAAGAGCGGGCAGGAGGTCAGAGGGGGCAGGCTCTCAGGA 10176

Qy 721 CGATGGAGGAGTCAGTCTGAGGCTGAAGAGGAGGAGGGCTCTCGAGCCGACGGCTGCA 780
Db 10177 CGATGGAGGAGTCAGTCTGAGGCTGAAGAGGAGGAGGGCTCTCGAGCCGACGGCTGCA 10236

Qy 781 AGCCCTCCAGAGAGCTGGAAGAGCGGGAGGAGGACCTCCACGAGCCCTCGACAGCAGAA 840
Db 10237 AGCCCTCCAGAGAGCTGGAAGAGCGGGAGGAGGAGGACCTCCACGAGCCCTCGACAGCAGAA 10296

Qy 841 GSCAGGCTGGCCCTTAGCCACCGGCCCATCTGCGACCTCGGCTCCGTCGTCATAG 900
Db 10297 GSCAGGCTGGCCCTTAGCCACCGGCCCATCTGCGACCTCGGCTCCGTCGTCATAG 10356

Qy 901 GAGGCGACCTCGCGCTGCGCTTCTTAGCATGAAGTGTGTGGGGATTTGCAGAAGCAACAGGA 960
Db 10357 GAGGCGACCTCGCGCTGCGCTTCTTAGCATGAAGTGTGTGGGGATTTGCAGAAGCAACAGGA 10416

Qy 961 AACCCTATGCATCTGTAATCTAGGATTTATTTCAAAACAAAGG 1001
Db 10417 AACCCTATGCATCTGTAATCTAGGATTTATTTCAAAACAAAGG 10457

RESULT 2
AR342806
LOCUS AR342806 15418 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 1 from patent US 6576464.
ACCESSION AR342806
VERSION AR342806.1 GI:33738009
KEYWORDS
SOURCE Unknown.
ORGANISM Unclasseified.
REFERENCE 1 (bases 1 to 15418)
AUTHORS Gold,J.D. and Lebkowski,J.S.
TITLE Methods for providing differentiated stem cells
JOURNAL Patent: US 6576464-A 1 10-JUN-2003;
Geron Corporation; Menlo Park, CA
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ORIGIN
Query Match 100.0%; Score 1001; DB 6; Length 15418;
Best Local Similarity 100.0%; Pred. No. 9.1e-272;
Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAAGACCCAGCATTTGGCACCCCTGGACATTTGCCACAGCCCTCGGAAATTCACGCTGAC 60
Db 9500 AAAAGACCCAGCATTTGGCACCCCTGGACATTTGCCACAGCCCTCGGAAATTCACGCTGAC 9559

Qy 61 TAGCGACATCATGTACACACTCCCGTCCAGCAGCCGACCCCGCTGTTTTTATTTTAAATAGC 120
Db 9560 TAGCGACATCATGTACACACTCCCGTCCAGCAGCCGACCCCGCTGTTTTTATTTTAAATAGC 9619

Qy 121 TACAAAGCAGGGAATCCCTGCTAAATGTCCTTTAAACAACTGGTTTAAACAAACGGGTC 180
Db 9620 TACAAAGCAGGGAATCCCTGCTAAATGTCCTTTTAAACAACTGGTTTAAACAAACGGGTC 9679

Qy 181 CATCCGACCGGTGGACAGTTCTCTCACAGTGAAGAGGAACATCGCTTTTATAAGCCCTGCA 240
Db 9680 CATCCGACCGGTGGACAGTTCTCTCACAGTGAAGAGGAACATCGCTTTTATAAGCCCTGCA 9739

Qy 241 GGCATCTCAAGGGAATTAACGTGAGTCAAACTGCCACCTCCATGGGATAGTACGACGAC 300
Db 9740 GGCATCTCAAGGGAATTAACGTGAGTCAAACTGCCACCTCCATGGGATAGTACGACGAC 9799

Qy 301 ATGCTCAAAAAGAAAGAAATTTACCCCATGCGCAGGGGAGTGGTTGGGGGGTTAAGGACGG 360
Db 9800 ATGCTCAAAAAGAAAGAAATTTACCCCATGCGCAGGGGAGTGGTTGGGGGGTTAAGGACGG 9859

Qy 361 TGGGGGACAGCTGGGGGCTACTGCACGACCTTTTACTTAAAGCCAGTTTCTCGTTCT 420
Db 9860 TGGGGGACAGCTGGGGGCTACTGCACGACCTTTTACTTAAAGCCAGTTTCTCGTTCT 9919

Qy 421 GATGGTATTGGCTCAGTTATGGGAGACTAACCATAGGGGAGTGGGATGGGGNACCCGG 480
Db 9920 GATGGTATTGGCTCAGTTATGGGAGACTAACCATAGGGGAGTGGGATGGGGNACCCGG 9979

Qy 481 AGGCTGTGCCATCTTTGCCATGCCCAGTGTCTCGGACGAGTAATGCTCTAGAGATGCC 540

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Query Match 100.0%; Score 1001; DB 6; Length 15418;			
Best Local Similarity 100.0%; Pred. No. 9.1e-272;			
Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
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Qy	181	CATCCGACCGGTGACAGTTCCTCACAGTGAAGGAAACATGCGCTTATAAGCCTGCA	240
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Qy	301	ATGCTCAAAAGAAAGAAATTTACCCCATGCGAGGGGAGTGGTTGGGGGTTAAGGACGG	360
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Qy	361	TGGGGGACGAGCTGGGGGCTACTGCACGACCTTTTACTTAAAGCCAGTTCCTGGTTCT	420
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Qy	841	GGCACGGCTGGCCCTTAGGCCCAACAGGGCCCATCTGTGAGCTCCGGCTCCGTGCCATAG	900
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Qy	901	GAGGGCACTCGCGCTGCCCTTTCTAGCATGAAGTGTGTGGGGAATTTGCAGAGCAACAGGA	960
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Qy	961	AACCCATGCATGTGAATCTAGGATTAATTTCAAACAAAGG	1001
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VERSION			
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;			
Homnidae; Homo.			
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REFERENCE			
GOLD, J.D. and LeBrowski, J.S.			
Differentiated cells suitable for human therapy			
PATENT: WO 0242445-A 1 30-MAY-2002;			
Geron Corporation (US)			
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DEFINITION Sequence 1 from Patent WO02053760.
ACCESSION AX498409
VERSION AX498409.1 GI:23343287
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 Irving, J.M. and Lebkowski, J.S.
Chimeric cytolytic viruses for cancer treatment
Patent: WO 02053760-A 1 11-JUL-2002;
Geron Corporation (US)
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DEFINITION Sequence 1 from Patent WO0242468.
ACCESSION AX504952
VERSION AX504952.1 GI:23386282
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Hominidae; Homo.
REFERENCE
1 Schiff, M.J.
Glycosyltransferase vectors for treating cancer
Patent: WO 0242468-A 1 30-MAY-2002;
Geron Corporation (US)
Location/Qualifiers
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Sequencing of Human Chromosome 5
Unpublished
2 (bases 1 to 161252)
DOE Joint Genome Institute.
Direct Submission
Submitted (14-MAR-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
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Project Information
Center Project Name: 451340
Center clone name: RPCI-11_117B23
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Summary Statistics
Consensus quality: 148939 bases at least Q40
Consensus quality: 156608 bases at least Q30
Consensus quality: 158826 bases at least Q20
Estimated insert size: 175000; agarose-fp estimation
Estimated insert size: 160452; sum-of-contigs estimation
Quality coverage: 7.26 in Q20 bases; agarose-fp estimation
Quality coverage: 7.92 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 9 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 3008: contig of 3008 bp in length
* 3009 3108: gap of unknown length
* 3109 9209: contig of 6101 bp in length
* 9210 9309: gap of unknown length
* 9310 15613: contig of 6304 bp in length
* 15614 15713: gap of unknown length
* 15714 23243: contig of 7530 bp in length
* 23244 23344: gap of unknown length
* 23344 39674: contig of 16331 bp in length
* 39675 39774: gap of unknown length
* 39775 60001: contig of 20227 bp in length
* 60002 60101: gap of unknown length
* 60102 85303: contig of 25202 bp in length
* 85304 85403: gap of unknown length
* 85404 117460: contig of 32057 bp in length
* 117461 117560: gap of unknown length
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ORIGIN

Query Match 100.0%; Score 1001; DB 14; Length 161252;
Best Local Similarity 100.0%; Pred. No. 1.1e-271;
Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAAGACCCAGCATTTGGACCCCTGGACATTTGGCCCAACAGCCCTGGGAATTCACGTGAC 60
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Db 140525 TACGCACATCATGTACACATCTCCGCTCCAGCAGCCGCCCCGCTGTTTATTTAAATAGC 140466

Qy 121 TACAAAGCAGGGAATCCCTGCTAAATGTCTTTTAAACAAACTGGTTAAACAAACGGGTC 180
Db 140465 TACAAAGCAGGGAATCCCTGCTAAATGTCTTTTAAACAAACTGGTTAAACAAACGGGTC 140406

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Db 140405 CATCCGACGCTGACAGTTCCTCACAGTGAAGAGAACATGCCGTTTATTAAGACCTGCA 140346

Qy 241 GGCATCTCAAGGGAATTAACGCTGAGTCAAACTGCCACCTCATGGGATAGTACGCAAC 300
Db 140345 GGCATCTCAAGGGAATTAACGCTGAGTCAAACTGCCACCTCATGGGATAGTACGCAAC 140286

Qy 301 ATGCTCAAAAAGAAAGAAATTTACCCCATGTCAGGGAGTGGTGGGGGTTAAAGACGG 360
Db 140285 ATGCTCAAAAAGAAAGAAATTTACCCCATGTCAGGGAGTGGTGGGGGTTAAAGACGG 140226

Qy 361 TGGGGGACAGAGCTGGGGGCTACTGCAACCTTTTACTAAAGCAGTTCCTGTTCT 420
Db 140225 TGGGGGACAGAGCTGGGGGCTACTGCAACCTTTTACTAAAGCAGTTCCTGTTCT 140166

Qy 421 GATGGTATTTGCTCAGTTATGGAGAGCTAACCATAGGGAGTGGGATGGGGGAACCCGG 480
Db 140165 GATGGTATTTGCTCAGTTATGGAGAGCTAACCATAGGGAGTGGGATGGGGGAACCCGG 140106

Qy 481 AGGCTGTGCCATCTTTGTCATGCCGAGTGTCTGGGAGGATTAATGCTCTAGAGATGCC 540
Db 140105 AGGCTGTGCCATCTTTGTCATGCCGAGTGTCTGGGAGGATTAATGCTCTAGAGATGCC 140046

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Db 139985 TGTGATCTCCGTGAGGACCTGAGTCTGGATCTTCCGACTACCTGACAGGCCCGAA 139926

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Qy 901 GAGGCACTCGCGCTGCCCTTTCTAGCATGAAGTGTGTGGGATTTGCAAGAGCAACAGGA 960
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Qy 961 AACCCATGCACTGTGAATCTAGGATTTATTTCAAAACAAAGG 1001
Db 139625 AACCCATGCACTGTGAATCTAGGATTTATTTCAAAACAAAGG 139585

RESULT 10
AX003120
LOCUS AX003120 5126 bp DNA linear PAT 24-AUG-2000
DEFINITION Sequence 1 from Patent WO9933998.
ACCESSION AX003120
VERSION AX003120.1 GI:9926982
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Wick,M. and Hagen,G.
TITLE Regulatory dna sequences of the human catalytic telomerase sub-unit
gene, diagnostic and therapeutic use thereof
JOURNAL Patent: WO 9933998-A 1 08-JUL-1999;
WICK MARESA (DE); BAYER AG (DE)
FEATURES
source
1. 5126
/organism="Homo sapiens"
/mol_type="unassigned DNA"
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ORIGIN

Query Match 98.7%; Score 988.4; DB 6; Length 5126;
Best Local Similarity 99.8%; Pred. No. 3e-268;
Matches 1000; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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Db 1139 TACGCACATCATGTACACATCTCCGCTCCAGCAGCCGCCCCGCTGTTTATTTAAATAGC 1198

Qy 121 TACAAAGCAGGGAATCCCTGCTAAATGTCTTTTAAACAAACTGGTTAAACAAACGGGTC 180
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Qy 181 CATCCGACGCTGACAGTTCCTCACAGTGAAGAGGAACATGCCGTTTATTAAGCCTGCA 240
Db 1259 CATCCGACGCTGACAGTTCCTCACAGTGAAGAGGAACATGCCGTTTATTAAGCCTGCA 1318

Qy 241 GGCATCTCAAGGGAATTAACGCTGAGTCAAACTGCCACCTCCATGGGATAGTACGCAAC 300
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Qy 301 ATGCTCAAAAAGAAAGAAATTTACCCCATGTCAGGGAGTGGTGGGGGTTAAAGACG 359
Db 1379 ATGCTCAAAAAGAAAGAAATTTACCCCATGTCAGGGAGTGGTGGGGGTTAAAGACG 1438

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Db 1439 GTGGGGGACGAGCTGGGGGCTACTGCAACCTTTTAAAGCCAGTTCCTGTTTC 1498

Qy 420 TGATGGTATTGGCTCAGTTATGGGAGACTAACCATAGGGAGTGGGATGGGGAACCCG 479
Db 1499 TGATGGTATTGGCTCAGTTATGGGAGACTAACCATAGGGAGTGGGGAACCCG 1558

Qy 480 GAGGCTGGCCATCTTTGCCATGCCGAGTGTCTGGGACAGATAATGCTCTAGAGATGC 539
Db 1559 GAGGCTGGCCATCTTTGCCATGCCGAGTGTCTGGGACAGATAATGCTCTAGAGATGC 1618

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Qy 660 AAGTAATCTCAGGGGTTCTCGGAGACAGCGCGGACAGAGGTCCAGAGGGGGGAGCCTCAGG 719
Db 1739 AAGTAATCTCAGGGGTTCTCGGAGAGAGCGGACAGAGGTCCAGAGGGGGGAGCCTCAGG 1798
Qy 720 ACGATGAGGACAGTCACTCTGAGGCTCAAAAGGAGGAGGAGGCGCTCGAGGCCAGCCTGC 779
Db 1799 ACGATGAGGACAGTCACTCTGAGGCTCAAAAGGAGGAGGAGGCGCTCGAGGCCAGCCTGC 1858
Qy 780 AAGGCCCTCCAGAGCTGGAAGAGCGGGAGAGGACCTCCACAGGAGCCTGCAGCAGGA 839
Db 1859 AAGGCCCTCCAGAGCTGGAAGAGCGGGAGAGGACCTCCACAGGAGCCTGCAGCAGGA 1918
Qy 840 AAGCAGCGCTGGCCCTTAGCCACACAGGCGCCATCGTGGACCTCCGGCCCTCGTGCCATA 899
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Db 2039 AAACCCATGCACTGTGAATCTAGGATTTTCAAAACAAAGG 2080

RESULT 11

AX003122 LOCUS AX003122 11276 bp DNA linear PAT 24-AUG-2000
DEFINITION Sequence 3 from Patent W09933998.
ACCESSION AX003122
VERSION AX003122.1 GI:9926984

KEYWORDS Homo sapiens (human)

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Homnidae; Homo.

REFERENCE

Wick, M. and Hagen, G.

Regulatory dna sequences of the human catalytic telomerase sub-unit

gene, diagnostic and therapeutic use thereof

Patent: W0 9933998-A 3 08-JUL-1999;

WICK MARESA (DE); BAYER AG (DE)

FEATURES

source

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/mol_type="unassigned DNA"

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ORIGIN

Query Match 98.7%; Score 988.4; DB 6; Length 11276;
Best Local Similarity 99.8%; Pred. No. 3.3e-268;
Matches 1000; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 1 AAAGACCCAGCATTTGGACCCCTGGACATTTGCCCCACAGCCCTGGGAATTCACGTGAC 60
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RESULT 12

AF114847

LOCUS

DEFINITION

Homo sapiens telomerase reverse transcriptase (TERT) gene, partial

cDS.

AF114847

ACCESSION

VERSION

AF114847.1

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Homnidae; Homo.

REFERENCE

AUTHORS

TITLE

Direct activation of TERT transcription by c-MYC

JOURNAL Nat. Genet. 21 (2), 220-224 (1999)
PUBMED 9988278
REFERENCE 2 (bases 1 to 12213)
AUTHORS Ducrest, A.-L., Amacker, M., Reichenbach, P., Nabholz, M. and Lingner, J.
TITLE Identification of the human telomerase reverse transcriptase (hTERT) promoter
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 12213)
AUTHORS Sutorisz, H., Palmquist, R., Roos, G., Stenling, R., Schorderet, D., Reddel, R., Lingner, J. and Nabholz, M.
TITLE Rearrangements of minisatellites in the human telomerase reverse transcriptase gene are not correlated with its expression in colon carcinomas
JOURNAL Unpublished
REFERENCE 4 (bases 1 to 12213)
AUTHORS Amacker, M., Simon-Vermot, N. and Lingner, J.
TITLE Direct Submission
JOURNAL Submitted (17-DEC-1998) Telomerase Research Unit, ISREC, Chemin de Boveresses 155, Epalinges 1066, Switzerland
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ORIGIN
Query Match 98.7%; Score 988.4; DB 8; Length 12213;
Best Local Similarity 99.8%; Pred. No. 3.3e-268;
Matches 1000; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
Qy 1 AAAAGCCCCAGCATGTGGACCCCTCGACATTTGGCCCCACAGCCCTGGGAATTCACGTGAC 60
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Db 4362 AAACCCATGCATGTGAATCTAGGATTTATTTCAAAAACAAAGG 4403

RESULT 13
HSTERT1
LOCUS Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-6. PRI 13-MAY-1999
DEFINITION
ACCESSION AF128893
VERSION AF128893.1 GI:4808970
KEYWORDS
SEGMENT
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 26414)
AUTHORS Wick, M., Zubov, D. and Hagen, G.
TITLE Genomic organization and promoter characterization of the gene encoding the human telomerase reverse transcriptase (hTERT)
JOURNAL Gene 232 (1), 97-106 (1999)
PUBMED 1033526
REFERENCE 2 (bases 1 to 26414)
AUTHORS Wick, M., Zubov, D. and Hagen, G.
TITLE Direct Submission
JOURNAL Submitted (16-FEB-1999) Dept. of Mol. Biol., Bayer AG Leverkusen, ZF-BTM, Bldg. Q18, Leverkusen D-51368, Germany
FEATURES
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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LOCUS								
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SOURCE	Homo sapiens (human)							
ORGANISM	Homo sapiens							
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.								
REFERENCE	1 (bases 1 to 202305)							
AUTHORS	DOE Joint Genome Institute and Stanford Human Genome Center.							
TITLE	Direct Submission							
JOURNAL	Unpublished							
AUTHORS	2 (bases 1 to 202305)							
TITLE	DOE Joint Genome Institute.							
JOURNAL	Direct Submission							
AUTHORS	Submitted (07-MAR-2002) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA							
TITLE	3 (bases 1 to 202305)							
JOURNAL	DOE Joint Genome Institute and Stanford Human Genome Center.							
AUTHORS	Submitted (15-MAR-2003) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA							
TITLE	On Mar 15, 2003 this sequence version replaced gi:19224940.							
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ORIGIN								

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 10, 2006, 10:27:39 ; Search time 205 seconds
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	1001	100.0	15418	3	US-09-244-438-1
4	1001	100.0	15418	3	US-09-995-419A-1
5	988.4	98.7	51552	3	US-09-733-294A-30
6	50.2	5.0	25589	3	US-09-949-002-716
7	49.2	4.9	32177	3	US-09-949-002-712
8	49	4.9	7218	2	US-08-232-463-14
9	48.2	4.8	93493	3	US-09-949-016-12063
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11	48	4.8	601	3	US-09-949-016-19450
12	48	4.8	601	3	US-09-949-016-19451
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15	47.8	4.8	134008	3	US-09-949-016-13841
16	47.4	4.7	601	3	US-09-949-016-71147
17	46.8	4.7	601	3	US-09-949-016-19449
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ALIGNMENTS

RESULT 1

US-09-783-203-1
; Sequence 1, Application US/09783203
; Patent No. 6576464
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Gold, Joseph
; APPLICANT: Lebkowski, Jane
; TITLE OF INVENTION: Tpacked stem cells
; FILE REFERENCE: 096/003
; CURRENT APPLICATION NUMBER: US/09/783,203
; CURRENT FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: 60/253,443
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/253,357
; PRIOR FILING DATE: 2000-11-27
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 15418
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-783-203-1

Query Match	100.0%;	Score 1001;	DB 3;	Length 15418;
Best Local Similarity	100.0%;	Pred. No. 2.6e-307;	Mismatches 0;	Indels 0;
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RESULT 2

US-09-994-427A-1
; Sequence 1, Application US/09994427A
; Patent No. 6713055
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Schiff, J. Michael
; TITLE OF INVENTION: GLYCOSYLTRANSFERASE VECTORS FOR TREATING CANCER
; FILE REFERENCE: 083,002
; CURRENT APPLICATION NUMBER: US/09/994,427A
; CURRENT FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: 60/253,395
; PRIOR FILING DATE: 2000-11-27
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 15418
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-994-427A-1

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Best Local Similarity 100.0%; Pred. No. 2.6e-307;

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; Patent No. 6921665				
; GENERAL INFORMATION:				
; APPLICANT: Geron Corporation				
; APPLICANT: McWhir, Jim				
; APPLICANT: Gold, Joseph D.				
; APPLICANT: Schiff, J. Michael				
; TITLE OF INVENTION: 096,004 - Seglist				
; FILE REFERENCE: 096,004 - Seglist				
; CURRENT APPLICATION NUMBER: US/09/995,419A				
; CURRENT FILING DATE: 2001-11-26				
; PRIOR APPLICATION NUMBER: 60/253,357				
; PRIOR FILING DATE: 2000-11-27				
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; SEQ ID NO 1				
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; TYPE: DNA				
; ORGANISM: Homo sapiens				
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Qy 9860 TGGGGGCGCAGCAGCTGGGGGCTACTGCAGCAGCACCCTTTACTAAAGCAGTTTCCCTGGTTCT 9919
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Qy 421 GATGGTATTGGCTCAGTTATGGGAGACTAAACATAGGGAGTGGGGATGGGGGAACCCGG 480
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Qy 9920 GATGGTATTGGCTCAGTTATGGGAGACTAAACATAGGGAGTGGGGATGGGGGAACCCGG 9979
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Qy 481 AGGCTGTGCCATCTTTGCGCATGCCGAGTGTCTTGGGCGAGGATATGCTCTAGAGATGCC 540
Db |||||
Qy 9980 AGGCTGTGCCATCTTTGCGCATGCCGAGTGTCTTGGGCGAGGATATGCTCTAGAGATGCC 10039
Db |||||
Qy 541 CACGTCCTGATTCCTCCCAAACTGTGCAGCAACCCCGCCGCGCCCTTTGAGG 600
Db |||||
Qy 10040 CACGTCCTGATTCCTCCCAAACTGTGCAGCAACCCCGCCGCGCCCTTTGAGG 10099
Db |||||
Qy 601 TGTGATCTCCGTGAGGACCTCTGAGGTCTGGGATCTTGGGACTACCTGCAGGCCCCGAAA 660
Db |||||
Qy 10100 TGTGATCTCCGTGAGGACCTCTGAGGTCTGGGATCTTGGGACTACCTGCAGGCCCCGAAA 10159
Db |||||
Qy 661 AGTAATCAGGGGTTCTGGGAAGAGCGGGCAGAGGGTCAAGGGGGCGAGCCTCAGGA 720
Db |||||
Qy 10160 AGTAATCAGGGGTTCTGGGAAGAGCGGGCAGAGGGTCAAGGGGGCGAGCCTCAGGA 10219
Db |||||
Qy 721 CGATGGAGGCACTCAGTCTGAGGCTGAAAGGGAGGAGGGCTCGAGGCCCGAGCCTGCA 780
Db |||||
Qy 10220 CGATGGAGGCACTCAGTCTGAGGCTGAAAGGGAGGAGGGCTCGAGGCCCGAGCCTGCA 10279
Db |||||
Qy 781 AGCCCTCCAGAACTGGAAGAGCGGGAGGAGGACCTCCACGGAGCTGCAGCAGGAA 840
Db |||||
Qy 10280 AGCCCTCCAGAACTGGAAGAGCGGGAGGAGGACCTCCACGGAGCTGCAGCAGGAA 10339
Db |||||
Qy 841 GGCAAGCTGGCCCTTAGCCCAACAGGGCCCATCGTGAGACCTCCGGCTTCGGTGCCATAG 900
Db |||||
Qy 10340 GGCAAGCTGGCCCTTAGCCCAACAGGGCCCATCGTGAGACCTCCGGCTTCGGTGCCATAG 10399
Db |||||
Qy 901 GAGGGCACTCGCGCTGCGCTTCTAGCATGAAGTGTGGGGATTTGCAAGAGCAACAGGA 960
Db |||||
Qy 10400 GAGGGCACTCGCGCTGCGCTTCTAGCATGAAGTGTGGGGATTTGCAAGAGCAACAGGA 10459
Db |||||
Qy 961 AACCATGCACTGTGAATCTAGGATTATTTCAAACAAAGG 1001
Db |||||
Qy 10460 AACCATGCACTGTGAATCTAGGATTATTTCAAACAAAGG 10500
Db |||||
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RESULT 5

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US-09-733-294A-30
; Sequence 30, Application US/09733294A
; Patent No. 6492171
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: William Gaarde
; APPLICANT: Susan M. Freier
; APPLICANT: Edward V. Wanciewicz
; TITLE OF INVENTION: ANTISENSE MODULATION OF TERT EXPRESSION
; FILE REFERENCE: ISFH-0527
; CURRENT APPLICATION NUMBER: US/09/733,294A
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 09/572,423
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 108
; SEQ ID NO 30
; LENGTH: 51552
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: exon
; LOCATION: (1)...(11492)
; OTHER INFORMATION: exon 1
; NAME/KEY: intron
; LOCATION: (11493)...(11596)
; OTHER INFORMATION: intron 1
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; NAME/KEY: exon
; LOCATION: (11597)...(12950)
; OTHER INFORMATION: exon 2
; NAME/KEY: intron
; LOCATION: (12951)...(21566)
; OTHER INFORMATION: intron 2
; NAME/KEY: exon
; LOCATION: (21567)...(21762)
; OTHER INFORMATION: exon 3
; NAME/KEY: intron
; LOCATION: (21763)...(23851)
; OTHER INFORMATION: intron 3
; NAME/KEY: exon
; LOCATION: (23852)...(24032)
; OTHER INFORMATION: exon 4
; NAME/KEY: intron
; LOCATION: (24033)...(24719)
; OTHER INFORMATION: intron 4
; NAME/KEY: exon
; LOCATION: (24720)...(24899)
; OTHER INFORMATION: exon 5
; NAME/KEY: intron
; LOCATION: (24900)...(25393)
; OTHER INFORMATION: intron 5
; NAME/KEY: exon
; LOCATION: (25394)...(25549)
; OTHER INFORMATION: exon 6
; NAME/KEY: intron
; LOCATION: (25550)...(30196)
; OTHER INFORMATION: intron 6
; NAME/KEY: exon
; LOCATION: (30195)...(30292)
; OTHER INFORMATION: exon 7
; NAME/KEY: intron
; LOCATION: (30293)...(31272)
; OTHER INFORMATION: intron 7
; NAME/KEY: exon
; LOCATION: (31273)...(31358)
; OTHER INFORMATION: exon 8
; NAME/KEY: intron
; LOCATION: (31359)...(33843)
; OTHER INFORMATION: intron 8
; NAME/KEY: unsure
; LOCATION: 31450
; OTHER INFORMATION: unknown
; NAME/KEY: exon
; LOCATION: (33844)...(33957)
; OTHER INFORMATION: exon 9
; NAME/KEY: intron
; LOCATION: (33958)...(35941)
; OTHER INFORMATION: intron 9
; NAME/KEY: exon
; LOCATION: (35942)...(36013)
; OTHER INFORMATION: exon 10
; NAME/KEY: intron
; LOCATION: (36014)...(37884)
; OTHER INFORMATION: intron 10
; NAME/KEY: exon
; LOCATION: (37885)...(38073)
; OTHER INFORMATION: exon 11
; NAME/KEY: intron
; LOCATION: (38074)...(41874)
; OTHER INFORMATION: intron 11
; NAME/KEY: exon
; LOCATION: (41875)...(42001)
; OTHER INFORMATION: exon 12
; NAME/KEY: intron
; LOCATION: (42002)...(42881)
; OTHER INFORMATION: intron 12
; NAME/KEY: exon
; LOCATION: (42882)...(42943)
; OTHER INFORMATION: exon 13
; NAME/KEY: intron
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LOCATION: (42944)...(46129)
OTHER INFORMATION: intron 13
NAME/KEY: exon
LOCATION: (46130)...(46254)
OTHER INFORMATION: exon 14
NAME/KEY: intron
LOCATION: (46255)...(47035)
OTHER INFORMATION: intron 14
NAME/KEY: exon
LOCATION: (47036)...(47173)
OTHER INFORMATION: exon 15
NAME/KEY: intron
LOCATION: (47174)...(47709)
OTHER INFORMATION: intron 15
NAME/KEY: exon
LOCATION: (47710)...(50544)
OTHER INFORMATION: exon 16
US-09-733-294A-30

Query Match 98.7%; Score 988.4; DB 3; Length 51552;
Best Local Similarity 99.8%; Pred. No. 5.2e-303; Indels 1; Gaps 1;
Matches 1000; Conservative 0; Mismatches 1;

Qy 1 AAAGACCCAGCATTTGGCACCCTCTGGACATTTGCCACAGCCCTGGGAATTCAGTGAC 60
Db 7229 AAAGACCCAGCATTTGGCACCCTCTGGACATTTGCCACAGCCCTGGGAATTCAGTGAC 7288

Qy 61 TAGCACAATCATGATACACATCTCCGTCACAGCCGACCCCGCTGTTTATTTAATAGC 120
Db 7289 TAGCACAATCATGATACACATCTCCGTCACAGCCGACCCCGCTGTTTATTTAATAGC 7348

Qy 121 TACAAGCGGGAATCCCTGCTAAATGTCCTTTTACAACTGTTTAAACAAAGGTC 180
Db 7349 TACAAGCGGGAATCCCTGCTAAATGTCCTTTTACAACTGTTTAAACAAAGGTC 7408

Qy 181 CATCGCACGCTGACAGTCTCTCACTGAAGAGGAACATGCCGTTTATAAGCCCTGCA 240
Db 7409 CATCGCACGCTGACAGTCTCTCACTGAAGAGGAACATGCCGTTTATAAGCCCTGCA 7468

Qy 241 GGCATCTCAAGGGAATTAACGTGATGATCAAACTGCCACCTCCATGGGATAGTACGCAAC 300
Db 7469 GGCATCTCAAGGGAATTAACGTGATGATCAAACTGCCACCTCCATGGGATAGTACGCAAC 7528

Qy 301 ATGCTCAAAAGAAAGAAATTTACCCCATGCGAGGAGTGTTT-GGGGGTTAAGACG 359
Db 7529 ATGCTCAAAAGAAAGAAATTTACCCCATGCGAGGAGTGTTT-GGGGGTTAAGACG 7588

Qy 360 GTGGGGGCGAGCAGCTGGGGGCTACTGACGACACCTTTTACTAAAGCCAGTTTCTGGTTC 419
Db 7589 GTGGGGGCGAGCAGCTGGGGGCTACTGACGACACCTTTTACTAAAGCCAGTTTCTGGTTC 7648

Qy 420 TGATGGTATTGGCTCAGTTATGGAGACTAAACATAGGGAGTGGGATGGGGAAACCCG 479
Db 7649 TGATGGTATTGGCTCAGTTATGGAGACTAAACATAGGGAGTGGGATGGGGAAACCCG 7708

Qy 480 GAGCTGTGCCATCTTTGCCATGCGCGAGTGTCTGGCAGAGTAATGCTCTAGATGC 539
Db 7709 GAGCTGTGCCATCTTTGCCATGCGCGAGTGTCTGGCAGAGTAATGCTCTAGATGC 7768

Qy 540 CCAGTCTCTGATTTCCCAACCTGTGGACAGAACCCGCGCCGCCAGGGCCCTTTGCGAG 599
Db 7769 CCAGTCTCTGATTTCCCAACCTGTGGACAGAACCCGCGCCGCCAGGGCCCTTTGCGAG 7828

Qy 600 GTGTGATCTCCGTGAGGACCTCTGAGGCTGGGATCTTTGGGACTTACCTGAGGCCCGAA 659
Db 7829 GTGTGATCTCCGTGAGGACCTCTGAGGCTGGGATCTTTGGGACTTACCTGAGGCCCGAA 7888

Qy 660 AAGTAATCCAGGGTTCTTGGGAAGAGGCGGCGAGAGGCTCAGAGGGGGGAGGCTCAGG 719
Db 7889 AAGTAATCCAGGGTTCTTGGGAAGAGGCGGCGAGAGGCTCAGAGGGGGGAGGCTCAGG 7948

Qy 720 ACGATGAGGCGATCAGTCTCAGGCTGAAAAGGGAGGAGGCGCTTCGAGGCCAGGCTGC 779

Db 7949 ACGATGAGGCGATCAGTCTCAGGCTGAAAAGGGAGGAGGGGCTTCGAGCCAGGCTGC 8008
Qy 780 AAGCGCTCCAGAGCTTGGAAAGCGGGAAGGGACCTTCCAGGAGCTTCAGCAGGA 839
Db 8009 AAGCGCTCCAGAGCTTGGAAAGCGGGAAGGGACCTTCCAGGAGCTTCAGCAGGA 8068
Qy 840 AAGCAGCGCTGGCCCTTTAGCCACACAGGCGCCATCGTGGACCTCCGCGCTCCGTCATA 899
Db 8069 AAGCAGCGCTGGCCCTTTAGCCACACAGGCGCCATCGTGGACCTCCGCGCTCCGTCATA 8128
Qy 900 GAGGGCAGCTCGCGCTGCCCTTCTAGCATGAGTGTGTGGGATTTTCAGAGCAACAGG 959
Db 8129 GAGGGCAGCTCGCGCTGCCCTTCTAGCATGAGTGTGTGGGATTTTCAGAGCAACAGG 8188
Qy 960 AAACCCATGACATGTAATCTAGGATTTATTTCAAAACAAAGG 1001
Db 8189 AAACCCATGACATGTAATCTAGGATTTATTTCAAAACAAAGG 8230

RESULT 6

US-09-949-002-716/c
Sequence 716, Application US/09949002
Patent No. 6900016
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL000790
CURRENT APPLICATION NUMBER: US/09/949,002
CURRENT FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: 60/231,401
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 10823
SOFTWARE: Fast-Seq for Windows Version 4.0
SEQ ID NO 716
LENGTH: 25589
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(25589)
OTHER INFORMATION: n = A,T,C or G
US-09-949-002-716

Query Match 5.0%; Score 50.2; DB 3; Length 25589;

Best Local Similarity 54.5%; Pred. No. 0.00017;
Matches 164; Conservative 0; Mismatches 133; Indels 4; Gaps 3;

Qy 591 CCTTTGCAAGTGTGATCTCGTGAGGACCCCTGAGGTCTGGGATCTTCGGGACTACCTGC 650
Db 927 CCTTGGCAGATATGATTAATTAAGATCTTGACAGAGAGCTATCTGGATATCTGG 868

Qy 651 AGGCCCGAAAAGTAATCCAGGGGTTCTGGGAAGAGCGGGCAGGAGGTTCAGAGGGGGC 710
Db 867 TGGACC-CAGTGTAACTCAGAGGGGCTTATTAGAGGGAGGCAAAAGGCTCAGAGTCAAGG 809

Qy 711 AG-CCTCAGGACGATGAGGCGATCAGTCTGAGGCTGAAAAGG--GAGGGAGGGCTCGA 767
Db 808 AGATGTCAATGGAAGCAAAAGGTTCAGATGATGATGCTTGTGTAAGAGGACATGA 749

Qy 768 GCCCAGGCTTCAGAGCCCTCCAGAGCTGGAAAAGCGGGAGGGACCTCCACGGAG 827
Db 748 GCCAAGGAACGAGATGGCTCTAGAACTAGAAAAGAGAGAACAGATTCTCTTAGAG 689

Qy 828 CCTCAGCAGGAAGGACGCGCTGGCCCTTAGCCACACAGGGGCCCATCTGTGACCTCCGGC 887
Db 688 CCTCAGAGGAACACACACACTTTGATTTACGCTGATAGGACACATTTTGGACTTCTGT 629

Qy 888 C 888
Db 628 C 628

Query Match 4.8%; Score 48.2; DB 3; Length 93493;
Best Local Similarity 56.2%; Pred. No. 0.0015;
Matches 131; Conservative 0; Mismatches 98; Indels 4; Gaps 2;

Qy 581 GGCCCCAGGCGCTTTGAGGTGTATCTCCGTGAGGACCTGAGGTCTGGATCCTTCGG 640
Db 22975 GGCAAAAAGGACTTTGAGAGGTGATCAAAATTAAGGACCTTGAATAAGAGGTAAGTCTG 22916

Qy 641 GACTACTCTGAGGCGCCGAAAGTAATCAGGGTTCTGGGAAGAGGGCGGAGGGGTC 700
Db 22915 GATTAGCTGGGTGACTCATTTATAATCAAGGGTCGGGGGCGCAGTAGGGTC--AATGTT 22858

Qy 701 AGAGGGGGGAGCTCAGGACGATGAGGAGGAGTCAGTCTGAGGCTGAAAGGAGGAGG 760
Db 22857 CGAGTAATGAGCATGAGAGGACCCCGGTAGCTATTGCTGGCTTTGAGATAGGGAAG 22798

Qy 761 G--CCTGAGCCAGGCGCTCGAAGCGCTCCAGAGCTGGAAAAGCGGGAA 811
Db 22797 GAACCAACAGACAAGAAATGCAATGCTCTACAAGCTGGAATGGAAGGAA 22745

RESULT 10
US-09-949-016-13272/c
; Sequence 13272, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13272
; LENGTH: 95020
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13272

Query Match 4.8%; Score 48.2; DB 3; Length 95020;
Best Local Similarity 56.2%; Pred. No. 0.0015;
Matches 131; Conservative 0; Mismatches 98; Indels 4; Gaps 2;

Qy 581 GGCCCCAGGCGCTTTGAGGTGTATCTCCGTGAGGACCTGAGGTCTGGATCCTTCGG 640
Db 23633 GGCAAAAAGGACTTTGAGAGGTGATCAAAATTAAGGACCTTGAATAAGAGGTAAGTCTG 23574

Qy 641 GACTACTCTGAGGCGCCGAAAGTAATCAGGGTTCTGGGAAGAGGGCGGAGGGGTC 700
Db 23573 GATTAGCTGGGTGACTCATTTATAATCAAGGGTCGGGGGCGCAGTAGGGTC--AATGTT 23516

Qy 701 AGAGGGGGGAGCTCAGGACGATGAGGAGGAGTCAGTCTGAGGCTGAAAAGGAGGAGG 760
Db 23515 CGAGTAATGAGCATGAGAACGACCCCGGTAGCTATTGCTGGCTTTGAGATAGGGAAG 23456

Qy 761 G--CCTGAGCCAGGCGCTCGAAGCGCTCCAGAGCTGGAAAAGCGGGGAA 811
Db 23455 GAACCAACAGACAAGAAATGCCAATGGCTCTACAAGCTGGAATGGAAGGAA 23403

RESULT 11
US-09-949-016-19450/c
; Sequence 19450, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19450
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-19450

Query Match 4.8%; Score 48; DB 3; Length 601;
Best Local Similarity 70.0%; Pred. No. 0.0001;
Matches 63; Conservative 1; Mismatches 26; Indels 0; Gaps 0;

Qy 751 GGGAGGAGGCGCTTCGAGCCCGAGCGCTTCAAGCGCTTCCAGAGCTGGAAAAGCGGGGA 810
Db 310 GGAAGGAGGCGCATGAGCCAGGCGGATGCGAGCACCTCCAGAGCTGGAAATTCAGGAA 251

Qy 811 AGGAGCCTCCAGGAGCGCTTCGAGCAGGAA 840
Db 250 AGGATCTCCCTGGAGCTTCCAGAAAGAA 221

RESULT 12

US-09-949-016-19451/c
; Sequence 19451, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19451
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-19451

Query Match 4.8%; Score 48; DB 3; Length 601;
Best Local Similarity 67.3%; Pred. No. 0.0001;
Matches 66; Conservative 1; Mismatches 31; Indels 0; Gaps 0;

Qy 743 GCTGAAAAGGAGGAGGCGCTTCGAGCCCGAGCGCTTCAAGCGCTTCCAGAGCTGGAAAA 802
Db 303 GCGGGCTTGAAGGAGGTCATGAGCCAGGCGGATGAGGACCTTCCAGAGCTGGAAATT 244

Qy 803 AGCGGGGAGGAGGACCTTCCAGCGGAGCTTCGAGCAGGAA 840
Db 243 GCCAGGAAGGGATCTCCCTGGAGCTTCCAGAAAGAA 206

RESULT 13
US-09-949-016-49663/c

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; Sequence 49663, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49663
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016--49663

Query Match      4.8%; Score 48; DB 3; Length 601;
Best Local Similarity 70.0%; Pred. No. 0.0001;
Matches 63; Conservative 1; Mismatches 26; Indels 0; Gaps 0;

Qy 751 GGAAGGAGGGCTCGAGCCAGCCGCTCGAAGCGCTCCAGAGCTGGAAGAAAGCGGGGA 810
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 310 GGAAGGAGGGKCCATGACGCCAGCGGATGCAGGCACCTCCAGAGCTGGAATTGCCAGAA 251
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 811 AGGACCCCTCCAGGAGCCTCGACGAGAA 840
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 250 AGGATCTCCCTCGAGCTCCAGAAAGAA 221
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 14
US-09-949-016-49664/c
; Sequence 49664, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49664
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-49664

Query Match      4.8%; Score 48; DB 3; Length 601;
Best Local Similarity 67.3%; Pred. No. 0.0001;
Matches 66; Conservative 1; Mismatches 31; Indels 0; Gaps 0;

Qy 743 GCTGAAAGGAGGAGGGCTCGAGCCAGCGCTCGAAGCGCTCCAGAGCTGGAAGAA 802
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 303 GCYGGCTTGAAGAGGTGCCATGAGCCAGGGATGCAGGCACTCCAGAGCTGGAATT 244
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 803 AGCGGGGAAGGAGCCCTCCAGGAGCTCGAGGAA 840
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 243 GCCAGGAAGAGGATCTCCCTCGAGCTTCAGAAAGAA 206
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 15
US-09-949-016-13841/c
; Sequence 13841, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13841
; LENGTH: 134008
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(134008)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13841

Query Match      4.8%; Score 47.8; DB 3; Length 134008;
Best Local Similarity 56.8%; Pred. No. 0.0024;
Matches 88; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

Qy 691 CAGGAGGGTTCAGAGGGGGGCGAGCCTCAGGACGATGAGGCGAGTCAGTCTCAGGCTGAAAA 750
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 55755 CACAAGAGGGATGGGGGGGGGGCTGTATCAGAGGGCGGTGACGTGAGACGGAGCGAGGC 55696
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 751 GGAAGGAGGGCTTCGAGCCAGCGCTCGAAGCGCTTCAGAGAGCTGGAAGAAAGCGGGGA 810
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 55695 TGGGGTGACTCAGGCGCTGCACCAAGGGCGAGCGGCTTCAGAGCTGGAAGAGCGGGAA 55636
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 811 AGGACCCCTCCAGGAGCCTCGACGAGGAGGCAC 845
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 55635 ACGGGGTCTCCCTGGAGCCCCCAGAAAGAACCCAC 55601
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Search completed: January 10, 2006, 19:47:31
Job time : 207 secs
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9800 ATGCTCAAAAGAGAAATTTACCCCATGGCAGGGAGTGGTTGGGG
 361 TGGGGGAGCAGCTGGGGGCTACTGACGACCTTTTAAAGAGCAGTGGGGGTTAAAGACGG 9859
 9860 TGGGGGAGCAGCTGGGGGCTACTGACGACCTTTTAAAGAGCAGTGGGGGTTAAAGACGG 420
 421 GATGGTATTTGGCTCAGTATAGGAGACTAAACATAGGAGGAGTGGGATCGTGGGGTCTTCT 9919
 9920 GATGGTATTTGGCTCAGTATAGGAGACTAAACATAGGAGGAGTGGGATCGTGGGGTCTTCT 480
 481 AGGCTGTGCATCTTTGGCANTGGCANTGGCANTGGCANTGGCANTGGCANTGGCANTGGCANTGG 9979
 9980 AGGCTGTGCATCTTTGGCANTGGCANTGGCANTGGCANTGGCANTGGCANTGGCANTGGCANTGG 540
 541 CAGTCTCTGATTTCCCAACCTGTGGACAGAACCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCG 10039
 10040 CAGTCTCTGATTTCCCAACCTGTGGACAGAACCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCG 600
 601 TGTGATCTCCGTGAGGACCTCTGAGGCTCTGGGATCTCTGGGATCTCTGGGATCTCTGGGATCT 10099
 10100 TGTGATCTCCGTGAGGACCTCTGAGGCTCTGGGATCTCTGGGATCTCTGGGATCTCTGGGATCT 660
 661 AGTAATCCAGGGGTTCTGGGAAAGAGCGCGGAGAGGGGCTGAGGAGGCTGAGGAGGCTGAGGAG 10159
 10160 AGTAATCCAGGGGTTCTGGGAAAGAGCGCGGAGAGGGGCTGAGGAGGCTGAGGAGGCTGAGGAG 720
 721 CGATGAGGAGCAGTCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 10219
 10220 CGATGAGGAGCAGTCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 780
 781 AGCGCTCCAGGAGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 10279
 781 AGCGCTCCAGGAGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 840
 10280 AGCGCTCCAGGAGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 10339
 841 GGCACGCTGGCCCTTGGCCACAGGCGCCCATCTGGTGGACCTCCGCGCTCCGCGCTCCGCGCTAG 900
 10340 GGCACGCTGGCCCTTGGCCACAGGCGCCCATCTGGTGGACCTCCGCGCTCCGCGCTCCGCGCTAG 10399
 901 GAGGCACTCGCGCTCCGCTTCTGACATGAGTGTGGGATTTGAGGATTTGAGGATTTGAGGATTT 960
 10400 GAGGCACTCGCGCTCCGCTTCTGACATGAGTGTGGGATTTGAGGATTTGAGGATTTGAGGATTT 10459
 961 AACCCATGCACTGTGAATCTAGGATTTTCAAAACAAAGG 1001
 10460 AACCCATGCACTGTGAATCTAGGATTTTCAAAACAAAGG 10500

RESULT 5
 US-10-023-969-1
 ; Sequence 1, Application US/10023969
 ; Publication No. US20030095989A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Geron Corporation
 ; APPLICANT: Irving, John
 ; APPLICANT: Lebkowski, Jane
 ; TITLE OF INVENTION: Chimeric Cytolytic Viruses for Cancer Treatment
 ; FILE REFERENCE: 084,002
 ; CURRENT APPLICATION NUMBER: US/10/023,969
 ; PRIOR FILING DATE: 2001-12-17
 ; PRIOR APPLICATION NUMBER: 60/256,418
 ; PRIOR FILING DATE: 2000-12-18
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 1
 ; LENGTH: 15418
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-023-969-1

Query Match 100.0%; Score 1001; DB 5; Length 15418;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 6
 US-10-206-447-1
 ; Sequence 1, Application US/10206447

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 9500 AAAAGAGCCAGCATTTGGCACCCCTGGACATTTGGCCCAACAGCCCTGGGATTTCACTGAC 955
 61 TACGACACATCATGTACACACTCCCTGTCACGACCGACCCCGCTGTTTAAATATAGC 120
 9560 TACGACACATCATGTACACACTCCCTGTCACGACCGACCCCGCTGTTTAAATATAGC 961
 121 TACAAAGCAGGGAATCCCTGCTAAATATGTCTTTAAACAACTGGTGTAAACAAACGGGTC 180
 9620 TACAAAGCAGGGAATCCCTGCTAAATATGTCTTTAAACAACTGGTGTAAACAAACGGGTC 967:
 181 CATCGCACGCTGGACAGTCTCTCAGTGAAGAGGAACATGCTCCCTTTTAAAGCCTTCA 240
 9680 CATCGCACGCTGGACAGTCTCTCAGTGAAGAGGAACATGCTCCCTTTTAAAGCCTTCA 973:
 241 GGCATCTCAAGGGGAATTTACGCTGAGTCAAACTGCTCCTCATATGGGATAGTACGCAAC 300
 9740 GGCATCTCAAGGGGAATTTACGCTGAGTCAAACTGCTCCTCATATGGGATAGTACGCAAC 9795
 301 ATGCTCAAAAGAAAGAAATTTACCCCATGSCAGGGAGTGGTGGGGGGTTAAAGACGG 360
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 361 TGGGGGAGCAGCTGGGGGCTACTGACGACCTTTTAAAGCAGTCTTCTGGTCT 420
 9860 TGGGGGAGCAGCTGGGGGCTACTGACGACCTTTTAAAGCAGTCTTCTGGTCT 9919
 421 GATGGTATTTGGCTCAGTATAGGAGACTAAACATAGGAGGAGTGGGATTTGAGGATTT 480
 9920 GATGGTATTTGGCTCAGTATAGGAGACTAAACATAGGAGGAGTGGGATTTGAGGATTT 9979
 481 AGGCTGTGCATCTTTGGCANTGGCANTGGCANTGGCANTGGCANTGGCANTGGCANTGGCANTGG 540
 9980 AGGCTGTGCATCTTTGGCANTGGCANTGGCANTGGCANTGGCANTGGCANTGGCANTGGCANTGG 1003:
 541 CAGCTCTGATTTCCCAACCTGTGGACAGAACCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCG 600
 10040 CAGCTCTGATTTCCCAACCTGTGGACAGAACCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCG 10095
 601 TGTGATCTCCGTGAGGACCTCTGAGGCTCTGGGATCTCTGGGATCTCTGGGATCTCTGGGATCT 660
 10100 TGTGATCTCCGTGAGGACCTCTGAGGCTCTGGGATCTCTGGGATCTCTGGGATCTCTGGGATCT 10159
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 721 CGATGAGGAGCAGTCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 780
 10220 CGATGAGGAGCAGTCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 10279
 781 AGCGCTCCAGGAGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 840
 10280 AGCGCTCCAGGAGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 10339
 841 GGCACGCTGGCCCTTGGCCACAGGCGCCCATCTGGTGGACCTCCGCGCTCCGCGCTCCGCGCTAG 900
 10340 GGCACGCTGGCCCTTGGCCACAGGCGCCCATCTGGTGGACCTCCGCGCTCCGCGCTCCGCGCTAG 10399
 901 GAGGCACTCGCGCTCCGCTTCTGACATGAGTGTGGGATTTGAGGATTTGAGGATTTGAGGATTT 960
 10400 GAGGCACTCGCGCTCCGCTTCTGACATGAGTGTGGGATTTGAGGATTTGAGGATTTGAGGATTT 10459
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 10460 AACCCATGCACTGTGAATCTAGGATTTTCAAAACAAAGG 10500

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721	CGATGGAGGCAGTCTGCTGAGGCTCGAAGGGAGGAGGGGCTCGAGCCCAAGGCTCGCA	781	AGCGCCTCCAGAAAGCTGGAAAAAGCGGGAGAGGACCTCCACGGAGCCTGCGACAGGAA	840	
Qy		Qy			
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Db		Db			
841	GGCACGGCTGGCCCTTAGCCCAACAGGGCCCATCGTGGACCTCCGGCCTCCGTGCCATAG	901	GAGGCACTGGCGCTGCCCTTCTAGCATGAAGTGTGTGGGATTTTCAGAGCAACAGGA	960	
Qy		Qy			
10340	GGCACGGCTGGCCCTTAGCCCAACAGGGCCCATCGTGGACCTCCGGCCTCCGTGCCATAG	10400	GAGGCACTGGCGCTGCCCTTCTAGCATGAAGTGTGTGGGATTTTCAGAGCAACAGGA	10410	
Db		Db			
901	GAGGCACTGGCGCTGCCCTTCTAGCATGAAGTGTGTGGGATTTTCAGAGCAACAGGA	961	AACCCATGCACTGGAACTTAGGATTAATTTCAAAACAAAGG	1001	
Qy		Qy			
10460	AACCCATGCACTGGAACTTAGGATTAATTTCAAAACAAAGG	10500			
Db		Db			

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RESULT 4
US-10-141-220-1
; Sequence 1, Application US/10141220
; Publication NO. US20030040111AI
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Gold, Joseph
; APPLICANT: Lebkowski, Jane
; TITLE OF INVENTION: Tracked stem cells
; FILE REFERENCE: 096/003
; CURRENT APPLICATION NUMBER: US/10/141,220
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: US/09/783,203
; PRIOR FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: 60/253,443
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/253,357
; PRIOR FILING DATE: 2000-11-27
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 15418
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-141-220-1

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[illegible]

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Db 9800 ATGCTCAAAAGAAGAAATTTACCCCATGCGAGGGAGTGTTTCTCTGTTCT 420
QY 361 TGGGGGCGAGAGCTGGGGGCTACTGACGACACTTTTACTAAGCGTTCCTGTTCT 9919
Db 9860 TGGGGGCGAGAGCTGGGGGCTACTGACGACACTTTTACTAAGCGCGTGGGACCGG 480
QY 421 GATGGTATTGGCTCAGTTATGGAGAGCTAAACATAGGGGAGTGGGGTATTAACCCGG 9979
Db 9920 GATGGTATTGGCTCAGTTATGGAGAGCTAAACATAGGGGAGTGGGGATGCGATGCC 540
QY 481 AGGCTGTGCCACTCTTTGCCATGCCCGAGTGTCTGGCGAGGATATGCTGATGCC 10039
Db 9980 AGGCTGTGCCACTCTTTGCCATGCCCGAGTGTCTGGCGAGGATATGCTGATGCC 600
QY 541 CAGCTCTGATTTCCCCCAAACCTGTGCGACAGAACCGGCGCGGCTTTGCGAGG 10099
Db 10040 CAGCTCTGATTTCCCCCAAACCTGTGCGACAGAACCGGCGCGGCTTTGCGAGG 660
QY 601 TGTGATCTCGTGAGGACCTCTGAGTCTTGGGATCCTTCTGAGGGGCGAGCTTCAGGA 720
Db 10100 TGTGATCTCGTGAGGACCTCTGAGTCTTGGGATCCTTCTGAGGGGCGAGCTTCAGGA 10219
QY 661 AGTAATCAGGGGTTCTGCGAAGAGCGCGGCGAGGCTTGGGAGAGCGGCTTCGAG 780
Db 10160 AGTAATCAGGGGTTCTGCGAAGAGCGCGGCGAGGCTTGGGAGAGCGGCTTCGAG 10279
QY 721 CGATGAGGCGAGTCAGTCTGAGGCTTGGGAGAGGCGGCTTCGAGCCAGGCTTCGA 10279
Db 10220 CGAGGCTTGGGAGAGCGGCGAGGCTTCGAGCCAGGCTTCGAGCAGGAA 840
QY 781 AGGCGCTTCAGAGCTTGGGAGAGCGGCGAGGCTTCGAGCCAGGCTTCGAGCAGGAA 10339
Db 840 AGGCGCTTCAGAGCTTGGGAGAGCGGCGAGGCTTCGAGCCAGGCTTCGAGCAGGAA 10339
QY 841 GGACAGGCTGGGCGCTTAGCCACCGAGGCGGCTTCGAGCCAGGCTTCGAGCAGGCTTCGAG 900
Db 900 GGACAGGCTGGGCGCTTAGCCACCGAGGCGGCTTCGAGCCAGGCTTCGAGCAGGCTTCGAG 900
QY 901 GAGGCGCACTCGGCTGCGCTTCTTAGCATGAAGTGTGTGGGATTTGCGAAGAACACAGGA 960
Db 10400 GAGGCGCACTCGGCTGCGCTTCTTAGCATGAAGTGTGTGGGATTTGCGAAGAACACAGGA 10459
QY 961 AACCCATGCACTGTGAATCTAGGATTTTCAAAACAAAGG 1001
Db 10460 AACCCATGCACTGTGAATCTAGGATTTTCAAAACAAAGG 10500

RESULT 8
US-10-811-012-1
; Sequence 1, Application US/10811012
; Publication No. US20040152189A1
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: McWhir, Jim
; APPLICANT: Gold, Joseph D.
; APPLICANT: Schiff, J. Michael
; TITLE OF INVENTION: Selective Antibody Targeting of Undifferentiated Stem Cells
; FILE REFERENCE: 096.0065- Seq1st
; CURRENT APPLICATION NUMBER: US/10/811,012
; CURRENT FILING DATE: 2004-03-26
; PRIOR APPLICATION NUMBER: 09/995,419
; PRIOR FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 60/253,357
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/253,443
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/253,395
; PRIOR FILING DATE: 2000-11-27
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 15418
; TYPE: DNA

; ORGANISM: Homo sapiens
 US-10-811-012-1

Query Match	100.0%	Score 1001	DB 7	Length 15418
Best Local Similarity	100.0%	Pred. No. 0		
Matches 1001	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY 1	AAAAGACCCAGCATTTGGCACCCCTGGACATTTGGCCACAGCCCTGGGAATTCACCTGAC	60		
DB 9500	AAAAGACCCAGCATTTGGCACCCCTGGACATTTGGCCACAGCCCTGGGAATTCACCTGAC	9559		
QY 61	TACGCACATCATGTACACATCTCCGCTCCAGACCGACCCCGCTGTTTTTAAATAGC	120		
DB 9560	TACGCACATCATGTACACATCTCCGCTCCAGACCGACCCCGCTGTTTTTAAATAGC	9619		
QY 121	TACAAAGCAGGGAATCCCTGCTAAATGTCCTTTAACCAACCTGGTTAAACAAACGGGTC	180		
DB 9620	TACAAAGCAGGGAATCCCTGCTAAATGTCCTTTAACCAACCTGGTTAAACAAACGGGTC	9679		
QY 181	CATCCGCACGGTGGACAGTTTCTCACAGTGAAGAGGAACAATGCCGTTTTTAAAGCCCTGCA	240		
DB 9680	CATCCGCACGGTGGACAGTTTCTCACAGTGAAGAGGAACAATGCCGTTTTTAAAGCCCTGCA	9739		
QY 241	GGCATCTCAAGGGAATTAAGCTGAGTCAAAAATGCGACCTCAATGGGATACGTAGCGCAAC	300		
DB 9740	GGCATCTCAAGGGAATTAAGCTGAGTCAAAAATGCGACCTCAATGGGATACGTAGCGCAAC	9799		
QY 301	ATGCTCAAAAAGAAAGAAATTTACCCCATGGCAGGGGAGTGGTTGGGGGTTTAAAGACGG	360		
DB 9800	ATGCTCAAAAAGAAAGAAATTTACCCCATGGCAGGGGAGTGGTTGGGGGTTTAAAGACGG	9859		
QY 361	TGGGGGACAGCTGGGGGCTACTGCAACGACCTTTTACTAAAGCCAGTTTCTGCTGTTCT	420		
DB 9860	TGGGGGACAGCTGGGGGCTACTGCAACGACCTTTTACTAAAGCCAGTTTCTGCTGTTCT	9919		
QY 421	GATGGTATTGGCTCAGTTATGGGAGCTAAACATAGGGGAGTGGGGATGGGGGAACCCGG	480		
DB 9920	GATGGTATTGGCTCAGTTATGGGAGCTAAACATAGGGGAGTGGGGATGGGGGAACCCGG	9979		
QY 481	AGGCTGTGCCATCTTTGCCATGCCCGAGTGCTCTGGCAGGATATGCTCTAGAGATGCC	540		
DB 9980	AGGCTGTGCCATCTTTGCCATGCCCGAGTGCTCTGGCAGGATATGCTCTAGAGATGCC	10039		
QY 541	CACGTCCTGATTTCCCCAAACCTGTGGAACGAACCCGCCGCCGCCCTTTGACAGG	600		
DB 10040	CACGTCCTGATTTCCCCAAACCTGTGGAACGAACCCGCCGCCGCCCTTTGACAGG	10099		
QY 601	TGTGATCTCGTGAGACCTCAGGTCTGGGATCTTGGGACTACTGCAAGGCCCGGAAA	660		
DB 10100	TGTGATCTCGTGAGACCTCAGGTCTGGGATCTTGGGACTACTGCAAGGCCCGGAAA	10159		
QY 661	AGTAATCCAGGGGTTCTGGGAAGAGCGCGGAGGAGGTCTAGAGGGGCGAGCCTCAGGA	720		
DB 10160	AGTAATCCAGGGGTTCTGGGAAGAGCGCGGAGGAGGTCTAGAGGGGCGAGCCTCAGGA	10219		
QY 721	CGATGAGGACGTCAGTCTGAGGCTGAAAAGGAGGAGGAGGCTCGAGCCCGAGGCTGCA	780		
DB 10220	CGATGAGGACGTCAGTCTGAGGCTGAAAAGGAGGAGGAGGCTCGAGCCCGAGGCTGCA	10279		
QY 781	AGGCGCTTCAGAGCTGGAAAAGCGGGGAAGGGAACCTTCCAAGGAGGCTCGAGCAGGAA	840		
DB 10280	AGGCGCTTCAGAGCTGGAAAAGCGGGGAAGGGAACCTTCCAAGGAGGCTCGAGCAGGAA	10339		
QY 841	GGCAGGCTGGCCCTTAGCCCAACAGGGGCCCATCGTGGACCTCCGGGCTCCGTCGCATAG	900		
DB 10340	GGCAGGCTGGCCCTTAGCCCAACAGGGGCCCATCGTGGACCTCCGGGCTCCGTCGCATAG	10399		
QY 901	GAGGGCACTTCGCGCTGCCCTTCTAGCATGAAGTGTGGGATTTGCAAGCAACAGGA	960		
DB 10400	GAGGGCACTTCGCGCTGCCCTTCTAGCATGAAGTGTGGGATTTGCAAGCAACAGGA	10459		
QY 961	AAACCATGCACTGTGAATCTAGGATTTTCAAACCAAGG	1001		

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Query Match	100.0%	Score 1001;	DB 5;	Length 15418;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1001;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	AAAAGACCCAGCATTTGGCACCCCTGGGACATTTGGCCCCACAGCCCTGGGGAATTCACGTGAC	60	
Db	9500	AAAAGACCCAGCATTTGGCACCCCTGGGACATTTGGCCCCACAGCCCTGGGGAATTCACGTGAC	9559	
Qy	61	TAGCCACATCATGTACACACATCCCGTCCACGACCGACCCCGCTGTTTTATTTTAAATAGC	120	
Db	9560	TAGCCACATCATGTACACACATCCCGTCCACGACCGACCCCGCTGTTTTATTTTAAATAGC	9619	
Qy	121	TACAAAGCAGGGAAATCCCTGCTAAAAATGTCCTTTAAACAAAATCGGTTAAACAAACCGGTC	180	
Db	9620	TACAAAGCAGGGAAATCCCTGCTAAAAATGTCCTTTAAACAAAATCGGTTAAACAAACCGGTC	9679	
Qy	181	CATCCGCAACGGTGGACAGTTCCCTCACAGTGAAGAGGAAATGCCCGTTTATAAGCCTCGCA	240	
Db	9680	CATCCGCAACGGTGGACAGTTCCCTCACAGTGAAGAGGAAATGCCCGTTTATAAGCCTCGCA	9739	
Qy	241	GGCATCTCAAGGGAAATTAACGCTGAGTCAAAATCGCATCCCTCATCGGATACCTACCGCAAC	300	
Db	9740	GGCATCTCAAGGGAAATTAACGCTGAGTCAAAATCGCATCCCTCATCGGATACCTACCGCAAC	9799	
Qy	301	ATGCTCAAAAAGAAAGAAATTTACCCCCATGCGAGGGAGTGGTTGGGGGGTTAAAGGACGG	360	

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